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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:42:53 ; Search time 168.444 Seconds
(without alignments)
93.904 Million cell updates/sec

Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKPAVLMMVFTYVGFNLGLTLILALISLFSIPVI 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	199	3 AAY71559	Aay71559 Rat Nogo
2	175	100.0	199	5 ABB81077	Abb81077 Rat Nogo
3	175	100.0	359	3 AAY71558	Aay71558 Rat Nogo
4	175	100.0	360	3 AAY71383	Aay71383 Rat Nogu
5	175	100.0	360	5 ABB81076	Abb81076 Rat Nogu
6	175	100.0	361	3 AAY71385	Aay71385 Alternati
7	175	100.0	379	7 ADB85283	Adb85283 Rat focce
8	175	100.0	403	3 AAY71563	Aay71563 Rat Nogo
9	175	100.0	522	3 AAY71312	Aay71312 Rat Nogu
10	175	100.0	1162	3 AAY71557	Aay71557 Mus muscu
11	175	100.0	1162	8 ADT89537	Adt89537 Mouse Nogu
12	175	100.0	1162	8 ADS99349	Ads99349 Mouse Nogu
13	175	100.0	1163	3 AAY71310	Aay71310 Rat Nogu
14	175	100.0	1163	5 ABB81074	Abb81074 Alternati
15	175	100.0	1163	8 ADO08105	Ado08105 Mouse pol
16	175	100.0	1163	8 ADO26399	Ado26399 Rat trunc
17	175	100.0	1163	8 ADP45572	Adp45572 Rat Nogu
18	175	100.0	1163	9 ADZ07609	Adz07609 Rat Nogu
19	175	100.0	1163	9 ADZ07609	Adz07609 Rat Nogu
20	174	99.4	175	2 AAW78194	Aaw78194 Human sec
21	174	99.4	199	2 AAW53947	Aaw53947 Human NSP
22	174	99.4	199	2 AAW78313	Aaw78313 Fragment
23	174	99.4	199	2 AAY35903	Aay35903 Extended
24	174	99.4	199	3 AAB12805	Aab12805 Human NSP

25	174	99.4	199	4 AAB82348	Aab82348 Human NOG
26	174	99.4	199	5 ABB81080	Abb81080 Human neu
27	174	99.4	199	7 ADK67504	Adk67504 Human RTN
28	174	99.4	199	8 ADP19211	Adp19211 Human sec
29	174	99.4	199	8 ADP67236	Adp67236 Human Nog
30	174	99.4	200	4 AAB64514	Aab64514 Human pol
31	174	99.4	291	4 AAM33484	Aam33484 Human pol
32	174	99.4	291	8 ADL31138	Adl31138 Human pro
33	174	99.4	373	3 AAY53624	Aay53624 A bone ma
34	174	99.4	373	3 AAY56969	Aay56969 Human MAG
35	174	99.4	373	3 AAB24242	Aab24242 Human NOG
36	174	99.4	373	3 AAB82350	Aab82350 Human NOG
37	174	99.4	373	5 AAM47954	Aam47954 Human RTN
38	174	99.4	373	5 ABG30937	Abg30937 Human pan
39	174	99.4	373	5 ABB68601	Abb68601 Human neu
40	174	99.4	373	5 ABB81079	Abb81079 Human apo
41	174	99.4	373	7 ADI63044	Adi63044 Human RTN
42	174	99.4	373	7 ADK67503	Adk67503 Human NOG
43	174	99.4	373	8 ADP67235	Adp67235 Human sec
44	174	99.4	642	2 AAW58383	Aaw58383 Human sec
45	174	99.4	642	4 AAB90682	Aab90682 Human BGI

ALIGNMENTS

RESULT 1

RAY71559
ID AAY71559 standard; protein, 199 AA.

XX AAY71559;

DT 02-NOV-2000 (first entry)

DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.
XX Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; mutain.

OS Rattus sp.

XX Key Location/Qualifiers
XX Region 1. .11

FT /note= "Corresponds to residues 40-50 of rat Nogo C
FT protein shown in AAY71312"

FT Region 12. .199
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"

WO200031235-A2.

PD 02-JUN-2000.

DP 05-NOV-1999; 99WO-US026160.

XX 06-NOV-1998; 98US-0107446P.

XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.

XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX Example; Page: 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic diseases of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, cranio-pharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutic which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments from rat Nogo C and Nogo A proteins.
CC The fragment is used in the construction of mutant Nogo-C which is
CC composed of His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NRH 3r3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo C sequence shown in AAY71312
CC and Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
XX Sequence 199 AA;
Query Match 100.0%; Score 175; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMWVFTYVGALENGLLTLLILALISLFSIPVI 36
DB 127 LKFAVLMWVFTYVGALENGLLTLLILALISLFSIPVI 162
RESULT 2
ABB81077
ID ABB81077 standard; protein; 199 AA.
XX
XX ABB81077;
XX
XX 05-NOV-2002 (first entry)
XX
XX Rat neurotransmitter receptor protein Nogo-C.
XX Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
XX central nervous system; peripheral nervous system; tranquilizer; Nogo;
XX vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
XX neurotropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
XX osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
XX neurotransmitter receptor; rat; receptor.
XX
XX Rattus norvegicus.
XX
XX US2002072493-A1.
XX
XX 13-JUN-2002.
XX
XX 28-JUN-2001; 2001US-00893348.
XX
XX 19-MAY-1998; 98IL-00124500.
XX
XX 21-JUL-1998; 98WO-US014715.
XX
XX 22-DEC-1998; 98US-00218277.
XX
XX 19-MAY-1999; 99US-00314161.
XX

PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
PI Moalem G;
XX
XX WPI; 2002-607255/65.
DR N-PSDB; ABB86600.
XX
XX Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
XX Example 5; Page 48-49; 93pp; English.
XX
XX The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischemic stroke or
CC damage caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or stroke. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A, and Igg gamma-
CC pathies, complications of various drugs (e.g. metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific
CC antigen
XX
XX Sequence 199 AA;
Query Match 100.0%; Score 175; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 3.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMWVFTYVGALENGLLTLLILALISLFSIPVI 36
DB 126 LKFAVLMWVFTYVGALENGLLTLLILALISLFSIPVI 161
RESULT 3
AAV71558
ID AAV71558 standard; protein; 359 AA.
XX
XX AAV71558;
XX
XX 02-NOV-2000 (first entry)
XX
XX Rat Nogo A protein fragment used in the construction of mutant Nogo-B.
XX
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening; mutant; mutein.

us-09-830-972a-2_copy_1090_1125.rag

Tue Feb 21 15:13:27 2006

XX OS Rattus sp.
XX FH Key Location/Qualifiers
XX FT Region 1. .171
XX FT /note= "Corresponds to residues 1-171 of rat Nogo A
XX FT protein shown in AAY71310"
XX FT Region 172. .359
XX FT /note= "Corresponds to residues 975-1162 of rat Nogo A
XX FT protein shown in AAY71310"
XX PN WO200031235-A2.
XX XX 02-JUN-2000.
XX PD 02-NOV-1999; 99WO-US026160.
XX PF 06-NOV-1998; 98US-0107446P.
XX PR (SCHW/) SCHWAB M E.
XX PA (CHEN/) CHEN M S.
XX PI Schwab ME, Chen MS;
XX XX WPI; 2000-400052/34.
XX DR Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX FT of the central nervous system and inducing regeneration of neurons.
XX PS Example; Page; 122pp; English.
XX CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC treatment of disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments of rat Nogo A protein shown in
CC AAY71310. The fragment is used in the construction of mutant Nogo-B. The
CC mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo A sequence shown in AAY71310.
CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC disclosure of the specification. However, the specification does not
CC include sequences for these SEQ ID numbers
XX SQ Sequence 359 AA;

Query Match 100.0%; Score 175; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 7.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMVFTYVGFALFNGLTLLILALISLFSIPVI 36
Db 287 LKFAVLMVFTYVGFALFNGLTLLILALISLFSIPVI 322

RESULT 4

XX AAY71383
XX ID AAY71383 standard; protein; 360 AA.
XX AC AAY71383;
XX DT 02-NOV-2000 (first entry)
XX DE Rat neurite growth inhibitor Nogo B.
XX KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; glioma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX OS Rattus sp.
XX FH Key Location/Qualifiers
XX FT Region 1. .172
XX FT /note= "Corresponds to amino acids 1-172 of Nogo A
XX FT protein shown in AAY71310"
XX FT Inhibitory-site 1. .171
XX FT /note= "Inhibits NIH 3T3 fibroblast spreading"
XX FT Modified-site 30
XX FT /note= "Casein kinase II site"
XX FT Region 31. .58
XX FT /note= "Acidic region"
XX FT Region 173. .360
XX FT /note= "Corresponds to C-terminal 188 amino acids
XX FT (residues 976-1163) of Nogo A protein (AAY71310). This
XX FT region is common to Nogo A, B and C isoforms"
XX FT Domain 185. .220
XX FT /label= "Transmembrane domain
XX FT /note= "C-terminal hydrophobic region"
XX FT Modified-site 221
XX FT /note= "Protein kinase C (PKC) site"
XX FT Modified-site 268. .270
XX FT /note= "Asn is N-glycosylated"
XX FT Modified-site 270. .286
XX FT /note= "Protein kinase C (PKC) site"
XX FT Modified-site 286
XX FT /note= "Protein kinase C (PKC) site"
XX FT Domain 287. .322
XX FT /label= "Transmembrane domain
XX FT /note= "C-terminal hydrophobic region"
XX FT Modified-site 338. .340
XX FT /note= "Asn is N-glycosylated"
XX FT Modified-site 340
XX FT /note= "Protein kinase C (PKC) site"
XX PN WO200031235-A2.
XX PD 02-JUN-2000.
XX XX 05-NOV-1999; 99WO-US026160.
XX PR 06-NOV-1998; 98US-0107446P.
XX PA (SCHW/) SCHWAB M E.
XX PA (CHEN/) CHEN M S.
XX PI Schwab ME, Chen MS;
XX XX WPI; 2000-400052/34.
XX PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX FT of the central nervous system and inducing regeneration of neurons.
XX PS Example; Page; 122pp; English.
XX CC The present sequence is a rat Nogo B protein which is a potent neural

protein shown in AAY71310"

Inhibitory-site
1. .171
/note= "Inhibits NIH 3T3 fibroblast spreading"

Modified-site
30
/note= "Casein kinase II site"

Region
31. .58
/note= "Acidic region"

Region
173. .361
/note= "Corresponds to amino acids 975-1163 of Nogo A"

Region
174. .361
/note= "This region is common to Nogo A, B and C isoforms"

Domain
186. .221
/label= "Transmembrane domain"
/note= "C-terminal hydrophobic region"

Modified-site
222
/note= "Protein kinase C (PKC) site"

Modified-site
269. .271
/note= "Asn is N-glycosylated"

Modified-site
271
/note= "Protein kinase C (PKC) site"

Modified-site
287
/note= "Protein kinase C (PKC) site"

Domain
288. .323
/label= "Transmembrane domain"
/note= "C-terminal hydrophobic region"

Modified-site
339. .341
/note= "Asn is N-glycosylated"

Modified-site
341
/note= "Protein kinase C (PKC) site"

W0200031235-A2.
02-JUN-2000.
05-NOV-1999; 99WO-US026160.
06-NOV-1998; 98US-0107446P.
(SCHW/) SCHWAB M E.
(CHEN/) CHEN M S.
Schwab ME, Chen MS;
WPI; 2000-400052/34.
Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.
Claim 4; Page; 122pp; English.
The present sequence is an alternative version of rat Nogo B protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The Nogo B transcript arises as a result of alternative splicing of Nogo gene. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence is not given in the specification but is derived from Nogo A protein sequence (AAY71310) and corresponds to

CC residues 1-172 fused to 975-1163 of Nogo A. This sequence is an
CC alternative version of the Nogo B sequence (see AAY71383) described in
CC the specification as being residues 1-172 fused to C-terminal 188 amino
CC acids (residues 975-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
CC Claim 32 and SEQ ID NO: 29 in disclosure of the specification. However
CC the specification does not include sequences for these SEQ ID numbers
XX
XX Sequence 361 AA;
SQ
Query Match 100.0%; Score 175; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.3e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGVGFNLTLILALISLFSIPVI 36
DB 288 LKFAVLMMVFTYVGVGFNLTLILALISLFSIPVI 323
RESULT 7
ADB85283
ID ADB85283 standard; protein; 379 AA.
XX
AC ADB85283;
XX
DT 04-DEC-2003 (first entry)
XX
DE Rat foocen-m2 reticulon SEQ ID NO:164.
XX
KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
KW protease; enzyme; analgesic; gene therapy; pain; diabetes.
XX
OS Rattus norvegicus.
XX
DN EP1284297-A2.
XX
DD 19-FEB-2003.
XX
FF 26-JUL-2002; 2002EP-00255228.
XX
PR 27-JUL-2001; 2001GB-00018354.
PR 07-FEB-2002; 2002GB-00002880.
XX
PA (WARN) WARNER LAMBERT CO.
XX
XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
PI
XX WPI; 2003-364994/35.
DR N-PSDB; ADB85284.
XX
XX Use of gene sequence that is down-regulated in response to streptozocin-
XX induced diabetes, vector, host cell, animal, polypeptide and antibody, in
XX screening of compounds for treating or diagnosing pain.
XX
XX Disclosure; Page 239-240; 256pp; English.
XX
XX The invention relates to a novel isolated gene sequence that is down-
XX regulated in the spinal cord in response to streptozocin-induced
XX diabetes, or comprising, hybridising or having at least 80% sequence
XX identity to a sequence whose expression products are kinases,
XX phosphatases, ion channel proteins, receptors, transporters, G-protein
XX coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
XX given in the specification. A gene of the invention has analgesic
XX activity, and may have a use in gene therapy. The gene sequences, vector,
XX host cell, animal, polypeptide and antibody are useful for screening of
XX compounds for diagnosing or treating pain. The kits are useful for
XX simultaneous separate or sequential detecting and/or quantifying down-
XX regulation of a gene sequence in the spinal cord of a mammal in response
XX to streptozocin-induced diabetes. The compound or pharmaceutical
XX composition is useful as a medicament for treating or diagnosing pain.
XX the present sequence represents a protein encoded by a gene of the
XX invention.

FT Misc-difference 371 /note= "Encoded by TAG"
 FT Misc-difference 371 /note= "Encoded by TGA"
 FT Misc-difference 374 /note= "Encoded by TAG"
 FT Misc-difference 380 /note= "Encoded by TAA"
 FT Misc-difference 406 /note= "Encoded by TAA"
 FT Misc-difference 408 /note= "Encoded by TAG"
 FT Misc-difference 410 /note= "Encoded by TAA"
 FT Misc-difference 422 /note= "Encoded by TAA"
 FT Misc-difference 433 /note= "Encoded by TGA"
 FT Misc-difference 440 /note= "Encoded by TAG"
 FT Misc-difference 453 /note= "Encoded by TAG"
 FT Misc-difference 455 /note= "Encoded by TAG"
 FT Misc-difference 482 /note= "Encoded by TAG"
 FT Misc-difference 513 /note= "Encoded by TAA"
 FT WO2000031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX WPI; 2000-400052/34.
 DR N-PSDB; RAD01175.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 PT
 PS Claim 7; Fig 14; 122pp; English.
 CC The present sequence is a rat Nogo C protein which is a potent neural
 CC cell growth inhibitor and is free of all central nervous system (CNS)
 CC myelin material with which it is natively associated. Nogo proteins and
 CC fragments displaying neurite growth inhibitory activity are used in the
 CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
 CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma, glioblastoma,
 CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
 CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
 CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
 CC activity can be used to treat or prevent hyperproliferative or benign
 CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
 CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
 CC production of Nogo protein to induce regeneration of neurons or to
 CC promote structural plasticity of the CNS in disorders where neurite
 CC growth, regeneration or maintenance are deficient or desired. The animal
 CC models can be used in diagnostic and screening methods for predisposition
 CC to disorders and to screen for or test molecules which can treat or
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
 CC these SEQ ID numbers
 XX Sequence 522 AA;
 SQ

Query Match 100.0%; Score 175; DB 3; Length 522;
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LKFAVIMVFTYVGALFNGLTLLILALISLFSIPVI 36
 DB 165 LKFAVIMVFTYVGALFNGLTLLILALISLFSIPVI 200
 RESULT 10
 AAY71557
 ID AAY71557 standard; protein; 1162 AA.
 XX
 AC AAY71557;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.
 XX
 OS Rattus sp.
 XX
 XX WO2000031235-A2.
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX WPI; 2000-400052/34.
 DR
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 PT
 PS Example; Page; 122pp; English.
 CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can
 CC be used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
 CC tag/77-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
 CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
 CC region was identified in the Nogo A sequence from amino acids 172-974.
 CC particularly amino acids 542-724. In addition, N-terminal region 1-171
 CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The

CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AA71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 1162 AA;
Query Match 100.0%; Score 175; DB 3; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125
RESULT 11
ADT89537
ID ADT89537 standard; protein; 1162 AA.
XX
AC ADT89537;
XX
DT 16-DEC-2004 (first entry)
XX
DE Mus musculus Nogo protein.
XX
KW Nerve regeneration; gene therapy; vaccine; neuroprotective; neurotropic;
KW Nogo; mouse.
XX
OS Mus musculus.
XX
PN US2004191240-A1.
XX
PD 30-SEP-2004.
XX
PF 31-JUL-2003; 2003US-00633423.
XX
PR 28-MAR-2003; 2003JP-00092923.
XX
PR 30-APR-2003; 2003US-00427741.
XX
PA (TOHY/) TOHYAMA M.
PA (YAMA/) YAMASHITA T.
XX
PI Tohyama M, Yamashita T;
XX
WPI; 2004-698659/68.
DR N-PSDB; ADT89536.
XX
PT Regenerating nerves or modulating nerve regeneration comprises inhibiting
PT or modulating p75 signal transduction pathway by administering a
PT transduction agent, e.g. p21 or Rho, or an agent that interacts with the
PT transduction agent.
XX
PS Example 2; SEQ ID NO 10; 209pp; English.
XX
CC The present invention relates to a method for regenerating nerves or
CC modulating nerve regeneration. The method involves inhibiting or
CC modulating a p75 signal transduction pathway. The invention is useful for
CC treating, preventing or diagnosing neurological diseases based on nerve
CC regeneration and for identifying agents useful for nerve regeneration.
CC The invention is also useful in gene therapy and for preparing vaccine.
CC The present sequence is the Mus musculus Nogo protein. Note: this
CC sequence is said to be encoded by SEQ ID NO 9, however this does not appear
CC to be the same.
XX
SQ Sequence 1162 AA;
Query Match 100.0%; Score 175; DB 8; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36

DB 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124
RESULT 12
ADS99349
ID ADS99349 standard; protein; 1162 AA.
XX
AC ADS99349;
XX
DT 30-DEC-2004 (first entry)
XX
DE Mouse Nogo protein - SEQ ID 10.
XX
KW nerve regeneration; neurological disease; Pep5; Rho GDI; Rho; Rho kinase;
KW disease; nervous disorder; nervous condition; spinal cord injury;
KW cerebrovascular disorder; brain injury; neurite outgrowth inhibition;
KW neuron network construction; Nogo.
XX
OS Mus musculus.
XX
PN WO2004087744-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-JP004385.
XX
PR 28-MAR-2003; 2003JP-00092923.
XX
PR 30-APR-2003; 2003JP-00125681.
XX
PR 31-JUL-2003; 2003JP-00284559.
XX
PA (INTE-) INTELLECTUAL PROPERTY CONSULTING INC.
XX
PI Tohyama M, Yamashita T, Tanaka H, Higuchi H;
XX
WPI; 2004-729217/71.
DR N-PSDB; ADS99348.
XX
PT New composition for regenerating nerves or treating neurological diseases
PT comprises a polypeptide (e.g. Pep5 or PKC) involved in p75 signal
PT transduction pathway, or an agent that interacts with the polypeptide to
PT block the pathway.
XX
PS Disclosure; SEQ ID NO 10; 613pp; English.
XX
CC The invention comprises a composition for regenerating nerves and
CC treating neurological diseases. The composition of the invention contains
CC a Pep5 polypeptide and an agent capable of interacting with a Rho GDI,
CC Rho, or Rho kinase polypeptide. The composition of the invention is
CC useful for treating, preventing, diagnosing, or prognosing nervous
CC disease/disorders/conditions, such as: spinal cord injury,
CC cerebrovascular disorders or brain injury. The composition of the
CC invention may also be used for disrupting or reducing inhibition of
CC neurite outgrowth or for constructing a network of neurons. In addition,
CC the composition may further be used to identify agents that may treat
CC neurological diseases or induce nerve regeneration. The present amino
CC acid sequence represents a mouse Nogo protein that was used in the
CC exemplification of the invention.
XX
SQ Sequence 1162 AA;
Query Match 100.0%; Score 175; DB 8; Length 1162;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
DB 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124
RESULT 13
AA71310
ID AA71310 standard; protein; 1163 AA.

CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence shown
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
XX Sequence 1163 AA;
SQ

Query Match 100.0%; Score 175; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 2,7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTTVGALFNGLTLLILALISLPSIPVI 36
DB 1090 LKFAVLMMVFTTVGALFNGLTLLILALISLPSIPVI 1125

RESULT 14
AAY71384
ID AAY71384 standard; protein; 1163 AA.
XX
AC AAY71384;
XX
DT 02-NOV-2000 (first entry)
XX
DE Alternative version of rat neurite growth inhibitor Nogo A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menigoma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX
XX
XX Key Location/Qualifiers
FH Inhibitory-site 1..171
FT Inhibitory-site /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT Region 31..58
FT Region /note= "Acidic region"
FT Region 172..259
FT Region /note= "This region is not essential for inhibitory
FT activity"
FT Misc-difference 223
FT /label= "Unknown
FT /note= "There is Leu at this position in the sequence
FT shown in AAY71310"
FT
FT Modified-site 233
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 242..244
FT /note= "Asn is N-glycosylated"
FT Modified-site 291
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 295
FT /note= "Protein kinase C (PKC) site"
FT Misc-difference 404
FT /note= "There is Ile at this position in the sequence
FT shown in AAY71310"
FT Modified-site 436
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 468..470

FT Misc-difference 469
FT /label= "Unknown
FT /note= "There is Lys at this position in the sequence
FT shown in AAY71310"
FT
FT Modified-site 484
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 488
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 502
FT /note= "Casein kinase II site"
FT Inhibitory-site 542..722
FT Modified-site 576
FT /note= "Casein kinase II site"
FT Peptide 623..640
FT /note= "used as immunogen to generate antibody AS 472"
FT Modified-site 626
FT /note= "Protein kinase C (PKC) site"
FT Misc-difference 661
FT /note= "There is Asn at this position in the sequence
FT shown in AAY71310"
FT Modified-site 694..696
FT /note= "Asn is N-glycosylated"
FT Modified-site 715
FT /note= "Casein kinase II site"
FT Peptide 762..1163
FT /note= "used as immunogen to generate antibody AS Bruna"
FT Modified-site 784
FT /note= "Protein kinase C (PKC) site"
FT Misc-difference 820
FT /note= "There is Leu at this position in the sequence
FT shown in AAY71310"
FT
FT Modified-site 821
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 850
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 855
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 863
FT /note= "Casein kinase II site"
FT Modified-site 868
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 893
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 912..914
FT /note= "Asn is N-glycosylated"
FT Modified-site 925..927
FT /note= "Asn is N-glycosylated"
FT Modified-site 954
FT /note= "PKC and casein kinase II sites"
FT Modified-site 956
FT /note= "PKC and casein kinase II sites"
FT Region 975..1162
FT /note= "This region is not essential for inhibitory
FT activity"
FT Region 976..1163
FT /note= "C-terminal common region found in Nogo A, B and C
FT isoforms"
FT Domain 988..1023
FT /label= "Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 1024
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 1071..1073
FT /note= "Asn is N-glycosylated"
FT Modified-site 1073
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 1089
FT /note= "Protein kinase C (PKC) site"
FT Domain 1090..1125
FT /label= "Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 1141..1143

us-09-830-972a-2_copy_1090_1125.rag

Tue Feb 21 15:13:27 2006

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 17, 2006, 03:49:55 ; Search time 25.7778 Seconds
(without alignment)
134.372 Million cell updates/sec
Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	85.7	208	160904	neuroendocrine-spe
2	150	85.7	267	A60021	tropomyosin-relate
3	150	85.7	776	A46583	neuroendocrine-spe
4	97	55.4	222	T26213	hypothetical prote
5	97	55.4	2484	T26216	hypothetical prote
6	97	55.4	2607	T26215	hypothetical prote
7	76.5	43.7	275	T05595	hypothetical prote
8	74.5	42.6	267	AD1561	B. subtilis YoaT p
9	70.5	40.3	267	AE1204	hypothetical prote
10	68	38.9	271	TI3013	hypothetical prote
11	66	37.7	255	E84899	hypothetical prote
12	62	35.4	183	A84527	probable membrane
13	61.5	35.1	236	A10142	Na+-transporting t
14	61	34.9	289	S12619	hypothetical prote
15	59.5	34.0	413	D71112	hypothetical prote
16	59	33.7	449	F89780	hypothetical prote
17	58.5	33.4	220	AG0337	probable membrane
18	57	32.6	557	T43657	probable glucosyl
19	56	32.0	325	T44365	cation-efflux syst
20	56	32.0	325	D90008	hypothetical prote
21	56	32.0	344	G72119	cytochrome D ubiq
22	56	32.0	344	H86503	cytochrome oxidase
23	55.5	31.7	234	B64815	ybH protein - Esc
24	55.5	31.7	234	A85587	hypothetical prote
25	55.5	31.7	234	H90736	hypothetical prote
26	54	30.9	213	H95174	amino acid ABC tra
27	54	30.9	232	A98041	hypothetical prote
28	54	30.9	281	S26018	NADH2 dehydrogenas
29	53.5	30.6	91	A12278	hypothetical prote

30	53	30.3	240	2	B82383	conserved hypothet
31	53	30.3	413	2	D84127	proton/sodium-glut
32	53	30.3	520	2	D70035	permease homolog y
33	52.5	30.0	292	2	H75055	hypothetical prote
34	52.5	30.0	373	2	H83891	spore germination
35	52.5	30.0	384	2	T11931	ubiquinol-cytochro
36	52.5	30.0	507	2	E90540	hypothetical prote
37	52.5	30.0	514	2	H87465	sodium-galactoside
38	52	29.7	242	2	H85016	hypothetical prote
39	52	29.7	268	2	D95302	hypothetical prote
40	52	29.7	459	2	T17175	NADH2 dehydrogenas
41	52	29.7	459	2	T17178	NADH2 dehydrogenas
42	52	29.7	610	2	H83243	probable ATP-bindi
43	52	29.7	610	2	H83243	deda protein - Esc
44	51.5	29.4	219	1	XMECAD	hypothetical prote
45	51.5	29.4	219	2	B85873	hypothetical prote

ALIGNMENTS

RESULT 1

I60904
neuroendocrine-specific protein C - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I60904
R:Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; V
J. Biol. Chem. 268, 13439-13447, 1993
A:Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-spec
A:Reference number: A45583; MUID:93293865; PMID:7685762
A:Accession: I60904
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-208 <RES>
A:Cross-references: UNIPROT:Q16799; UNIPARC:UPI000002B2DE; GB:L10335; NID:G307310; PIDN:
C:Genetics: NSFP
A:Gene: GDB:RTN1; NSFP
A:Cross-references: GDB:203968; OMIM:600865
A:Map position: 14q21-14q22

Query Match 85.7%; Score 150; DB 2; Length 208;
Best Local Similarity 72.2%; Pred. No. 9.5e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
|||||: |||||||||: |||: |||:
Db 135 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 170

RESULT 2

A60021
tropomyosin-related protein, neuronal - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C:Accession: A60021
R:Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A:Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A:Reference number: A60021; MUID:91278684; PMID:1647480
A:Accession: A60021
A:Molecule type: mRNA
A:Residues: 1-267 <RES>
A:Cross-references: UNIPARC:UPI0000086535; EMBL:X52817; NID:9456549; PIDN:CAA37001.1; PII
C:Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropo

Query Match 85.7%; Score 150; DB 2; Length 267;
Best Local Similarity 72.2%; Pred. No. 1.2e-10;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
|||||: |||||||||: |||: |||:
Db 126 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 161

```
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; UNIPARC:UPI00000827B8; EMBL:Z78066; PIDN:CAB51467.1;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 55.4%; Score 97; DB 2; Length 2484;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2403 IKFGLVMSLTYYIASWFSGFTLAILGLGVFSVPKV 2438

RESULT 6
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; UNIPARC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 55.4%; Score 97; DB 2; Length 2607;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2526 IKFGLVMSLTYYIASWFSGFTLAILGLGVFSVPKV 2561

RESULT 7
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q5SUR3; UNIPARC:UPI00000822F; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A:Note: F9D16.100
Query Match 43.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 40.5%; Pred. No. 0.059;
Matches 15; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; UNIPARC:UPI00000827B8; EMBL:Z78066; PIDN:CAB51467.1;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 55.4%; Score 97; DB 2; Length 2484;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2403 IKFGLVMSLTYYIASWFSGFTLAILGLGVFSVPKV 2438

RESULT 6
T26215
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; UNIPARC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 55.4%; Score 97; DB 2; Length 2607;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2526 IKFGLVMSLTYYIASWFSGFTLAILGLGVFSVPKV 2561

RESULT 7
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q5SUR3; UNIPARC:UPI00000822F; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A:Note: F9D16.100
Query Match 43.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 40.5%; Pred. No. 0.059;
Matches 15; Conservative 9; Mismatches 10; Indels 3; Gaps 1;

submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2484 <WIL>
A:Cross-references: UNIPROT:Q9U347; UNIPARC:UPI00000827B8; EMBL:Z78066; PIDN:CAB51467.1;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3c
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2
Query Match 55.4%; Score 97; DB 2; Length 2484;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2403 IKFGLVMSLTYYIASWFSGFTLAILGLGVFSVPKV 2438

RESULT 6
T26215
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: UNIPROT:Q23187; UNIPARC:UPI000007623E; EMBL:Z78066; PIDN:CAB01522.2;
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2
Query Match 55.4%; Score 97; DB 2; Length 2607;
Best Local Similarity 41.7%; Pred. No. 0.0015;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2526 IKFGLVMSLTYYIASWFSGFTLAILGLGVFSVPKV 2561

RESULT 7
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
A:Accession: T05595
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-275 <BEV>
A:Cross-references: UNIPROT:Q5SUR3; UNIPARC:UPI00000822F; EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:Introns: 89/1; 149/2; 196/3; 220/1
A:Note: F9D16.100
Query Match 43.7%; Score 76.5; DB 2; Length 275;
Best Local Similarity 40.5%; Pred. No. 0.059;
Matches 15; Conservative 9; Mismatches 10; Indels 3; Gaps 1;
```

QY 2 KPAVL---MWVTVVGVLFNGTLTLILALISLSPV 35
 DB 193 KFLIAIAGLWVILGCGCFNLTAYIALVLLFTVPL 229

RESULT 8
 A:Accession: AD1561
 B. subtilis YoaT protein homolog lin1029 [imported] - Listeria innocua (strain Clip11262)
 C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
 C:Accession: AD1561
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, R.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1561
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <GLA>
 A:Cross-references: UNIPROT:Q92CZ2; UNIPARC:UPI00000CC42E; GB:AL592022; PIDN:CAC96260.1
 A:Experimental source: strain Clip11262
 C:Genetics:
 A:Gene: lin1029
 C:Superfamily: membrane protein

Query Match 42.6%; Score 74.5; DB 2; Length 267;
 Best Local Similarity 46.2%; Pred. No. 0.098;
 Matches 18; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 1 LKPAVLMMWVTVVGA---LFGNLTLLILALISLSPV 36
 DB 1 MKPFRLLWVFTWKQALCCLFPFGIIFISLALTKLIDIPFI 39

RESULT 9
 A:Accession: AE1204
 B. subtilis YoaT protein homolog lmo1037 [imported] - Listeria monocytogenes (strain EGD)
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004
 C:Accession: AE1204
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, R.; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AE1204
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-267 <GLA>
 A:Cross-references: UNIPROT:Q8Y880; UNIPARC:UPI0000054DF1; GB:NC_003210; PIDN:CAC99115.1
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1037
 C:Superfamily: membrane protein

Query Match 40.3%; Score 70.5; DB 2; Length 267;
 Best Local Similarity 43.6%; Pred. No. 0.29;
 Matches 17; Conservative 6; Mismatches 13; Indels 3; Gaps 1;

QY 1 LKPAVLMMWVTVVGA---FNGLTLLILALISLSPV 36
 DB 1 MQPFRLLWVFTWKQALCCIFPGIIFISLALTKLIDIPFI 39

RESULT 10

TI3013
 hypothetical protein F8L21.10 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: TI3013
 R:Pevan, M.; Peters, S.A.; van Staveren, M.; Dickse, W.; Stiekema, W.; Bancroft, I.; Mew
 submitted to the Arabidopsis Protein Sequence Database, July 1999
 A:Reference number: Z17587
 A:Accession: TI3013
 A:Molecule type: DNA
 A:Residues: 1-271 <EV>
 A:Cross-references: UNIPROT:Q9SUT9; UNIPARC:UPI00000ACS1D; EMBL:AL096882; GSPDB:GN00062;
 A:Experimental source: cultivar Columbia; BAC clone F8L21
 C:Genetics:
 A:Gene: ATSP:F8L21.10
 A:Map position: 4
 A:Introns: 85/1; 145/2; 192/3; 216/1

Query Match 38.9%; Score 68; DB 2; Length 271;
 Best Local Similarity 37.9%; Pred. No. 0.58;
 Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 7 MWVTVVGVLFNGLTLLILALISLSPV 35
 DB 197 LWVLSILGCGCYFLLTAYIALVLLFTVPL 225

RESULT 11
 E84899
 hypothetical protein At2g46170 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84899
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84899
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-255 <STO>
 A:Cross-references: UNIPROT:O82352; UNIPARC:UPI00000A0AB3; GB:AE002093; NID:g3702332; PII
 C:Genetics:
 A:Gene: At2g46170
 A:Map position: 2

Query Match 37.7%; Score 66; DB 2; Length 255;
 Best Local Similarity 33.3%; Pred. No. 0.96;
 Matches 12; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 LKPAVLMMWVTVVGVLFNGLTLLILALISLSPV 36
 DB 174 LMVVVGLWITSVGVGNFNLTVYICFVILHTVPL 209

RESULT 12
 A84527
 hypothetical protein At2g15280 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A84527
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-183 <STO>

us-09-830-972a-2_copy_1090_1125.rpr

Tue Feb 21 15:13:28 2006

A:Cross-references: UNIPROT:Q9SHU8; UNIPARC:UPI00000A63C8; GB:AB002093; NID:G462633; PID: A:Gene: At2g15280
 C:Genetics:
 A:Map position: 2

Query Match 35.4%; Score 62; DB 2; Length 183;
 Best Local Similarity 31.4%; Pred. No. 2.1;
 Matches 11; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 KFAVLMMVFTVVGALFNGLTLLILALISLPSIPV 36
 DB 103 RVSVLMTVSPVGNFLTLVGLVLSLLPL 137

RESULT 13
 A:Title: Probable membrane protein YP01163 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A10142
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: A10142
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-236 <KUR>
 A:Cross-references: UNIPROT:Q8ZGW1; UNIPARC:UPI00000DCA1F; GB:AL590842; PIDN:CAC90004.1;
 C:Genetics:
 A:Gene: YP01163
 C:Superfamily: Escherichia coli ybhL protein

Query Match 35.1%; Score 61.5; DB 2; Length 236;
 Best Local Similarity 63.6%; Pred. No. 3;
 Matches 14; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 1 LKFAVLMMVFTVVGAL-FNGLT 21
 DB 163 LKSPALMMVFTVIGLVFVGLT 184

RESULT 14
 A:Title: Na⁺-transporting two-sector ATPase (EC 3.6.3.15) [similarity] - Propionigenium modestum
 C:Species: Propionigenium modestum
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 31-Dec-2004
 C:Accession: S12619; S12611; S29035; S23334; S24367; S36000
 R:Kaim, G.; Ludwig, W.; Dimroth, P.; Schleifer, K.H.
 Nucleic Acids Res. 18, 6697, 1990
 A:Title: Sequence of subunits a and b of the sodium ion translocating adenosine triphosph
 A:Reference number: S12619; MUID:91067471; PMID:2174545
 A:Accession: S12619
 A:Molecule type: DNA
 A:Residues: 1-289 <KAI>
 A:Cross-references: UNIPROT:P21903; UNIPARC:UPI000012632F; EMBL:X54809; NID:G45607; PIDN
 R:Esser, U.; Krumholz, L.R.; Simoni, R.D.
 Nucleic Acids Res. 18, 5887, 1990
 A:Title: Nucleotide sequence of the F(0) subunits of the sodium dependent F(1)F(0) ATPase
 A:Reference number: S12611; MUID:91016937; PMID:2170948
 A:Accession: S12611
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-113, 'I', 115-289 <ESS>
 A:Cross-references: UNIPARC:UPI000016FD91; EMBL:X53960; NID:G45643; PIDN:CAA37911.1; PID
 R:Krumholz, L.R.; Esser, U.; Simoni, R.D.
 FEBS Microbiol. Lett. 91, 37-42, 1992
 A:Title: Characterization of the genes coding for the F(1)F(0) subunits of the sodium de
 A:Reference number: S29034
 A:Accession: S29035
 A:Molecule type: DNA

A:Residues: 1-113, 'I', 115-287 <KRU1>
 A:Cross-references: UNIPARC:UPI0000175ED5; EMBL:X58461
 R:Krumholz, L.R.
 submitted to the EMBL Data Library, March 1991
 A:Reference number: S23333
 A:Accession: S23334
 A:Molecule type: DNA
 A:Residues: 1-113, 'I', 115-289 <KRU2>
 A:Cross-references: UNIPARC:UPI000016FD91; EMBL:X58461; NID:G897797; PIDN:CAA41368.1; PID
 R:Kaim, G.; Ludwig, W.; Dimroth, P.; Schleifer, K.H.
 Eur. J. Biochem. 207, 463-470, 1992
 A:Title: Cloning, sequencing and in vivo expression of genes encoding the F(0) part of th
 A:Reference number: S24366; MUID:92339434; PMID:11386022
 A:Accession: S24367
 A:Molecule type: DNA
 A:Residues: 1-95, 'L', 97-157, 'T', 158-205, 'L', 207-224, 'F', 226-289 <KAW>
 A:Cross-references: UNIPARC:UPI0000175ED6; EMBL:X66102
 R:Ludwig, W.
 submitted to the EMBL Data Library, May 1992
 A:Reference number: S36000
 A:Accession: S36000
 A:Molecule type: DNA
 A:Residues: 1-289 <LUD>
 A:Cross-references: UNIPARC:UPI000012632F; EMBL:X66102; NID:G45599; PIDN:CAA46894.1; PID:
 C:Genetics:
 A:Gene: uncB
 C:Superfamily: H(+)-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; blocked amino end; hydrolase; membrane-associated complex;

Query Match 34.9%; Score 61; DB 2; Length 289;
 Best Local Similarity 56.0%; Pred. No. 4.1;
 Matches 14; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 10 FTVVGALFNGLTLLILALISLPSIP 34
 DB 126 FTVIGTLF--LFLISNIVSFPIIP 148

RESULT 15
 D71112
 hypothetical protein PH0667 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C:Accession: D71112
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: D71112
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-413 <KAW>
 A:Cross-references: UNIPROT:O58400; UNIPARC:UPI0000062E95; GB:AP000003; NID:G3236130; PID
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0667

Query Match 34.0%; Score 59.5; DB 2; Length 413;
 Best Local Similarity 38.7%; Pred. No. 8.5;
 Matches 12; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 2 KFAVLMMVFTVVGALFNGLTLLILALISLPS 32
 DB 308 KLAILGILTFIGYAW-ATTIIMALVSLLS 337

Search completed: February 17, 2006, 03:56:52
 Job time : 26.7778 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:43:13 ; Search time 164.444 Seconds
(without alignments)
154.453 Million cell updates/sec

Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKFAVLMMVFTYGVGALFNLILALISLFSIPVI 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	100.0	199	1 RTN4 MOUSE	Q9972 mus musculus
2	175	100.0	199	2 Q8H51 MOUSE	Q7851 mus musculus
3	175	100.0	356	2 Q8H78 MOUSE	Q8H78 mus musculus
4	175	100.0	357	2 Q8K37 MOUSE	Q8K37 mus musculus
5	175	100.0	360	2 Q6IR3 RAT	Q6IR3 rattus norv
6	175	100.0	375	2 Q8H55 MOUSE	Q8H55 mus musculus
7	175	100.0	378	2 Q5403 RAT	Q5403 rattus norv
8	175	100.0	578	2 Q8095 MOUSE	Q8095 mus musculus
9	175	100.0	639	2 Q8K290 MOUSE	Q8K290 mus musculus
10	175	100.0	1046	2 Q8GK7 MOUSE	Q8GK7 mus musculus
11	175	100.0	1162	2 Q8GK9 MOUSE	Q8GK9 mus musculus
12	175	100.0	1163	1 RTN4 RAT	Q3J11 rattus norv
13	175	100.0	1163	2 Q8K38 MOUSE	Q8K38 mus musculus
14	175	100.0	1245	2 Q5DTK9 MOUSE	Q5DTK9 mus musculus
15	174	99.4	187	2 Q53Y1 HUMAN	Q53Y1 homo sapien
16	174	99.4	187	2 Q6IG5 PIG	Q6IG5 sus scrofa
17	174	99.4	193	2 Q6IF5 XENTR	Q6IF5 xenopus tro
18	174	99.4	194	2 Q4F22 MACMU	Q4F22 macaca mula
19	174	99.4	198	2 Q4F28 SHEEP	Q4F28 ovis aries
20	174	99.4	199	2 Q7L7Q5 HUMAN	Q7L7Q5 homo sapien
21	174	99.4	199	2 Q5R4X9 POMPY	Q5R4X9 pongo pygma
22	174	99.4	199	2 Q6IM70 PIG	Q6IM70 sus scrofa
23	174	99.4	199	2 Q7YR9 BOVIN	Q7YR9 bos taurus
24	174	99.4	199	2 Q4F293 PANTR	Q4F293 pan troglod
25	174	99.4	199	2 Q7T224 CHICK	Q7T224 gallus gall
26	174	99.4	199	2 Q4F284 XENTR	Q4F284 xenopus tro
27	174	99.4	315	2 Q6IFV4 XENTR	Q6IFV4 xenopus tro
28	174	99.4	326	2 Q4F283 CHICK	Q4F283 gallus gall
29	174	99.4	334	2 Q4F285 XENTR	Q4F285 xenopus tro
30	174	99.4	343	2 Q6IPN0 HUMAN	Q6IPN0 homo sapien
31	174	99.4	345	2 Q4F282 CHICK	Q4F282 gallus gall

32	174	99.4	373	2 Q7L7Q6 HUMAN	Q7L7Q6 homo sapien
33	174	99.4	392	2 Q9EB16 HUMAN	Q9EB16 homo sapien
34	174	99.4	459	2 Q4Z80 XENTR	Q4Z80 xenopus tro
35	174	99.4	538	2 Q5SS8 CHICK	Q5SS8 gallus gall
36	174	99.4	1086	2 Q8IUA4 HUMAN	Q8IUA4 homo sapien
37	174	99.4	1165	2 Q5MAJ0 CHICK	Q5MAJ0 gallus gall
38	174	99.4	1192	1 RTN4 HUMAN	Q9NCJ3 homo sapien
39	174	99.4	1192	2 Q7L7Q8 HUMAN	Q7L7Q8 homo sapien
40	171	97.7	139	2 Q6CM33 MACFA	Q6CM33 macaca fasc
41	171	97.7	193	2 Q6JRV6 XENLA	Q6JRV6 xenopus lae
42	171	97.7	193	2 Q6JRV6 XENLA	Q6JRV6 xenopus lae
43	171	97.7	199	2 Q7PCJ7 MACFA	Q7PCJ7 macaca fasc
44	171	97.7	199	2 Q6JRW3 XENLA	Q6JRW3 xenopus lae
45	171	97.7	199	2 Q6PB23 XENLA	Q6PB23 xenopus lae

ALIGNMENTS

RESULT 1
RTN4 MOUSE
ID RTN4 MOUSE STANDARD; PRT; 199 AA.
AC Q99F72; Q9CTE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN Name=Retn4; Synonyms=Nogo;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
[1]
RN NUCLEOTIDE SEQUENCE
RC STRAIN=313-Li; TISSUE=adipocyte;
RA Coulson A.C., Craggs P.D., Morris N.J.;
RT "Mouse vp20/RTN4C cDNA."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 170-199.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petkovski N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo L.G., Wagner L., Whitehead C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa I., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Shibata D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults (By
CC similarity).
CC -|- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC membrane of the endoplasmic reticulum through 2 putative
CC transmembrane domains (By similarity).
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms may be produced;
CC Name=1;
CC IsoId=Q9P72-1; Sequence=Displayed;
CC -|- SIMILARITY: Contains 1 reticulon domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed
CC -----
CC EMBL; AF326337; AAK08076.1; -; mRNA.
CC EMBL; AK003859; -; NOT ANNOTATED CDS; mRNA.
CC Ensembl; ENSMUSG0000020458; Mus musculus.
CC MGI; MGI-1915835; Rtn4
CC GO; GO:042895; C-cell projection; IDA.
CC GO; GO:0043025; C-cell soma; IDA.
CC GO; GO:0005783; C:endoplasmic reticulum; IDA.
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
CC GO; GO:0005635; C:nuclear membrane; ISS.
CC GO; GO:0005225; C:nuclear binding; ISS.
CC GO; GO:0001825; P:angiogenesis; IMP.
CC GO; GO:0019967; P:negative regulation of anti-apoptosis; ISS.
CC GO; GO:0030517; P:negative regulation of axon extension; ISS.
CC GO; GO:0007399; P:neurogenesis; IDA.
CC InterPro; IPR003386; Reticulon.
CC PANTHER; PTHR10994; Reticulon; 1.
CC Pfam; PF04503; Reticulon; 1.
CC PROSITE; PS50845; RETICULON; 1.
CC KW Alternative splicing; Endoplasmic reticulum; Transmembrane.
FT TOPO_DOM 1 25 Cytoplasmic (Potential).
FT TRANSMEM 26 50 Potential.
FT TOPO_DOM 51 137 Luminal (Potential).
FT TRANSMEM 138 162 Potential.
FT TOPO_DOM 163 199 Cytoplasmic (Potential).
FT DOMAIN 12 199 Reticulon.
FT SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;
Query Match 100.0%; Score 175; DB 1; Length 199;
Best Local Similarity 100.0%; Pred.No. 4.9e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKFAVLMMVFTYVVGALFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLMMVFTYVVGALFNGLTLLILALISLFSIPVI 161
RESULT 2
ID Q78NS1_MOUSE PRELIMINARY; PRT; 199 AA.
AC Q78NS1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RTN4 (Reticulon 4).
GN Name=Rtn4; ORFNames=RP23-17605.4-009;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVCJ7, and 129/SvcJ7;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RA MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RA "Genomic structure and functional characterisation of the promoters of
RA human and mouse nogo/rtn4.";
RA J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kay M.;
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102286; AAM73510.1; -; Genomic_DNA.
DR EMBL; AY102286; AAM73505.1; -; mRNA.
DR EMBL; AL929371; CAI24275.1; -; Genomic_DNA.
SQ SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;
Query Match 100.0%; Score 175; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 4.9e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKFAVLMMVFTYVVGALFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLMMVFTYVVGALFNGLTLLILALISLFSIPVI 161
RESULT 3
Q8BH78_MOUSE PRELIMINARY; PRT; 356 AA.
ID Q8BH78;
AC Q8BH78;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RTN4 (Reticulon 4).
GN Name=Rtn4; ORFNames=RP23-17605.4-007;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7, and 129SVCJ7;
RA MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RA "Genomic structure and functional characterisation of the promoters of
RA human and mouse nogo/rtn4.";
RA J. Mol. Biol. 325:299-323 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kay M.;
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102281; AAM73503.1; -; mRNA.
DR EMBL; AY102286; AAM73508.1; -; Genomic_DNA.
DR EMBL; AL929371; CAI24272.1; -; Genomic_DNA.
DR Ensembl; ENSMUSG0000020458; Mus musculus.

DR MGI:1915835; Rtn4.
DR GO:0042995; C:cell projection; IDA.
DR GO:0043025; C:cell soma; IDA.
DR GO:0005783; C:endoplasmic reticulum; IDA.
DR GO:0005515; F:protein binding; IPI.
DR GO:0001525; P:angiogenesis; IMP.
DR GO:0007399; P:neurogenesis; IDA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 100.0%; Score 175; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 7.5e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 283 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 318

RESULT 4
ID Q8K3G7_MOUSE PRELIMINARY; PRT; 357 AA.
AC Q8K3G7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nogo-B.
OS Name=Rtn4;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Jin W., Li R., Long M., Shen J., Ju G.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY114153; AA077069.1; -; mRNA.
DR MGI: MGI:1915835; Rtn4.
DR GO:0042995; C:cell projection; IDA.
DR GO:0043025; C:cell soma; IDA.
DR GO:0005783; C:endoplasmic reticulum; IDA.
DR GO:0005515; F:protein binding; IPI.
DR GO:0001525; P:angiogenesis; IMP.
DR GO:0007399; P:neurogenesis; IDA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 100.0%; Score 175; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 7.5e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 284 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 319

RESULT 5
ID Q6IRL3_RAT PRELIMINARY; PRT; 360 AA.
AC Q6IRL3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Rtn4 protein (Rtn4-B1).
GN Name=Rtn4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung; 8574 Placenta;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wegner L., Shenmen C.W., Schuler G.D.,
Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Mada A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22715887; PubMed=12832288;
RA Certle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT "A reticular rhapody: phylogenetic evolution and nomenclature of the
RTN/Nogo gene family";
RL FASEB J. 17:1238-1247(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC070879; AAH0879.1; -; mRNA.
DR EMBL: AY164740; AAP47315.1; -; mRNA.
DR EMBL: BC097936; AAH97936.1; -; mRNA.
DR GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro: IPR003388; Reticulon.
DR Pfam: PF02453; Reticulon; 1.
DR PROSITE: PS50845; RETICULON; 1.
SQ SEQUENCE 360 AA; 38822 MW; 149714AD6C3D65A7 CRC64;

Query Match 100.0%; Score 175; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.6e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 287 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 322

RESULT 6
ID Q8BHF5_MOUSE PRELIMINARY; PRT; 375 AA.
AC Q8BHF5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Rtn4 (Reticulon 4).
GN Name=Rtn4; ORFNames=RP23-17605.4-006;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Zhang C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gumatatne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettaman M., Madan A.C., Shevchenko Y., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.C., Trichmond J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.W., Grimwood J., Schmutz J., Skalka U., Smallus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RC Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC032192; AAH32192.1; -; mRNA.
DR MG1; MGI:1915835; Rtn4.
DR GO; GO:0042995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007389; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF0453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
DR SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;
SQ
Query Match 100.0%; Score 175; DB 2; Length 639;
Best Local similarity 100.0%; Fred. No. 1.1e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps
QY 1 LKFAVLMMVFTYVGALPFGNLTLILALISLSPVPI 36
DB 566 LKFAVLMMVFTYVGALPFGNLTLILALISLSPVPI 601
RESULT 10
ID Q8BGK7 MOUSE PRELIMINARY; PRT; 1046 AA.
AC Q8BGK7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RTN4 (Reticulon 4).
GN Name=Rtn4; ORFNames=RP23-17605.4-008;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
PY [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129/SVCJ7; and 1295vcj7;
EX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Gerlino T., Huber C., van der Putten H., Schwab M.E.,
RA "Genomic structure and functional characterization of the promoters of
RT human and mouse nogo/rtn4";
RT J. Mol. Biol. 325:299-323 (2003).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129/SVCJ7;
RC Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=1295vcj7;
RC

RA	Van der Putten H., Mir A.;
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	NUCLEOTIDE SEQUENCE.
RR	Kay M.;
RA	Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY102280; AAAM73502.1; -; mRNA.
DR	EMBL; AY102286; AAAM73507.1; -; Genomic DNA.
DR	EMBL; AL924371; CAI24274.1; -; Genomic DNA.
DR	Ensembl; ENSMUSG0000020458; Mus musculus.
DR	MGI; MGI:1915835; Rtn4
DR	GO; GO:0042895; C:cell projection; IDA.
DR	GO; GO:0043925; C:cell body; IDA.
DR	GO; GO:0005783; F:endoplasmic reticulum; IDA.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	GO; GO:0001525; P:angiogenesis; IMP.
DR	GO; GO:0007399; P:neurogenesis; IDA.
DR	InterPro; IPRO003388; Reticulon.
DR	Pfam; PF02453; Reticulon.1.
DR	PROSITE; PS0845; RETICULON; 1.
SQ	SEQUENCE 1046 AA; 114221 MW; 8CE2B2238ED51222 CRC64;
Query Match 100.0%; Score 175; DB 2; Length 1046;	
Best Local Similarity 100.0%; Pred. No. 1.6e-11;	
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 LKFAVLMWVTYVGALFNGLTLLILALISLSIPVI 36
DD	973 LKFAVLMWVTYVGALFNGLTLLILALISLSIPVI 1008
RESULT 11	
CS	C8EGMS_MOUSE PRELIMINARY; PRT; 1162 AA.
ID	C8EGMS_MOUSE PRELIMINARY; PRT; 1162 AA.
AC	C8EGMS; 2003 (TREMBLrel_23, Created)
DT	01-MAR-2003 (TREMBLrel_23, Last sequence update)
DT	01-MAR-2003 (TREMBLrel_23, Last sequence update)
DT	10-MAY-2005 (TREMBLrel_30, Last annotation update)
DE	RTN4 (Reticulon 4).
GN	Name=Rtn4; ORNames=RP23-17605.4--005;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
OX	[1]
PN	NUCLEOTIDE SEQUENCE.
RP	STRAIN=129/SVCJ7, and 129SvCj7;
RC	MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RX	Oertle T., Huber C., van der Putten H., Schwab M.B.;
RT	"Genomic structure and functional characterisation of the promoters of
RT	human and mouse nogo/rtn4.";
RN	J. Mol. Biol. 325:299-323(2003).
RN	[2]
PP	NUCLEOTIDE SEQUENCE.
RP	STRAIN=129/SVCJ7;
RA	Van der Putten H.;
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=129SVCJ7;
RC	STRAIN=129SVCJ7;
RA	Van der Putten H., Mir A.;
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	NUCLEOTIDE SEQUENCE.
RR	Kay M.;
RA	Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY102284; AAAM73506.1; -; mRNA.
DR	EMBL; AY102286; AAAM73511.1; -; Genomic DNA.
DR	EMBL; AL929371; CAI24273.1; -; Genomic DNA.
DR	Ensembl; ENSMUSG0000020458; Mus musculus.
DR	MGI; MGI:1915835; Rtn4
DR	GO; GO:0042995; C:cell projection; IDA.

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ID Q8K3G8_MOUSE PRELIMINARY; PRT; 1163 AA.
AC Q8K3G8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nogo-A.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Jin W., Long M., Li R., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114152; AAM77068.1; -; mRNA.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0043995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005151; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 1163 AA; 126690 MW; 685F362799417EA4 CRC64;
Query Match 100.0%; Score 175; DB 2; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125
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ID QSDTK9_MOUSE PRELIMINARY; PRT; 1245 AA.
AC QSDTK9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE MKTAA4153 protein (Fragment).
GN Name=Rtn4; Synonym=mkTAA4153;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Fetal Brain;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Nagase T., Ohara O.,
RA Koga H.;
RL "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
RT The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.",
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK220511; BAD90301.1; -; mRNA.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0042995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005151; P:protein binding; IPI.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
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Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1172 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1207
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ID Q53SV1_HUMAN PRELIMINARY; PRT; 187 AA.
AC Q53SV1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein RTN4 (Fragment).
GN Name=RTN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Maupin R., Haakenson W., Boyer E., Kang K.;
RL "The sequence of Homo sapiens BAC clone Rp11-56013.",
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC013414; AAY24239.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 187 AA; 20936 MW; A161F7A143C4607C CRC64;
Query Match 99.4%; Score 174; DB 2; Length 187;
Best Local Similarity 97.2%; Pred. No. 6.1e-12;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 114 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 149
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Job time : 165.444 secs

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us-09-830-972a-2_copy_1090_1125.ra1

Tue Feb 21 15:13:27 2006

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 17, 2006, 03:56:08 ; Search time 38.2222 Seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174	99.4	199	1	US-08-700-607-1
2	174	99.4	201	2	US-09-949-016-9124
3	150	85.7	208	1	US-08-700-607-7
4	150	85.7	267	1	US-08-700-607-6
5	150	85.7	356	1	US-08-700-607-6
6	150	85.7	439	2	US-09-949-016-9180
7	150	85.7	776	1	US-08-700-607-5
8	150	85.7	776	2	US-09-949-016-6998
9	136	77.7	219	2	US-09-270-767-45132
10	131	74.9	92	2	US-09-149-476-411
11	131	74.9	168	2	US-09-149-476-563
12	131	74.9	192	2	US-09-949-016-8859
13	124	70.9	241	1	US-08-700-607-3
14	120	68.6	588	2	US-09-949-016-7290
15	61.5	35.1	242	2	US-09-489-039A-12517
16	60.5	34.6	117	2	US-08-973-068-5
17	59	33.7	289	2	US-09-540-236-2019
18	57.5	32.9	242	2	US-09-489-039A-13008
19	56	32.0	268	2	US-09-198-452A-121
20	56	32.0	349	2	US-09-438-185A-105
21	55.5	31.7	744	2	US-09-785-381-1
22	55.5	31.7	744	2	US-09-785-381-3
23	54.5	31.1	970	2	US-09-795-927-7
24	54	30.9	213	2	US-09-583-110-3395
25	54	30.9	342	2	US-09-134-001C-4190
26	54	30.9	363	2	US-09-248-796A-17364
27	54	30.9	470	2	US-09-543-681A-4625

28	54	30.9	483	2	US-09-134-000C-4234
29	53.5	30.6	316	2	US-09-252-991A-21088
30	52	29.7	597	2	US-09-252-991A-32657
31	52	29.7	624	2	US-09-252-991A-21625
32	51.5	29.4	114	2	US-08-134-000C-6136
33	51	29.1	213	2	US-08-605-703B-2594
34	51	29.1	361	1	US-08-015-751-36
35	51	29.1	541	2	US-08-198-452A-692
36	51	29.1	544	2	US-08-138-185A-655
37	50.5	28.9	145	2	US-09-252-991A-29264
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39	50.5	28.9	342	2	US-09-134-000C-5431
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42	50	28.6	187	2	US-09-902-540-9915
43	50	28.6	234	2	US-09-107-532A-4817
44	50	28.6	355	2	US-09-170-496D-2
45	50	28.6	355	2	US-09-170-496D-164

ALIGNMENTS

RESULT 1
US-08-700-607-1
Sequence 1, Application US/08700607
Patent No. 5858708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-700-607-1

Query Match 99.4%; Score 174; DB 1; Length 199;
Best Local Similarity 97.2%; Pred. No. 6.1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36

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Sequence 21088, A
Sequence 32657, A
Sequence 21625, A
Sequence 6136, Ap
Sequence 2594, Ap
Sequence 36, Appl
Sequence 692, App
Sequence 655, App
Sequence 29264, A
Sequence 4246, A
Sequence 5431, Ap
Sequence 16020, A
Sequence 5457, Ap
Sequence 9915, Ap
Sequence 4817, Ap
Sequence 2, Appl
Sequence 164, App


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RESULT 5
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
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US-08-700-607-6
Query Match      85.7%; Score 150; DB 1; Length 356;
Best Local Similarity 72.2%; Pred. No. 1.4e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLLTLILALISLPSIPVI 36
Db      283 LKFAVLMMLLTYVGALFNGLLTLILMAVVSMTFLPVV 318

RESULT 6
US-09-949-016-9180
; Sequence 9180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 9180
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9180

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Best Local Similarity 72.2%; Pred. No. 1.7e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLLTLILALISLPSIPVI 36
Db      366 LKFAVLMMLLTYVGALFNGLLTLILMAVVSMTFLPVV 401

RESULT 7
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
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US-08-700-607-5
Query Match      85.7%; Score 150; DB 1; Length 776;
Best Local Similarity 72.2%; Pred. No. 3.2e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTYVGALFNGLLTLILALISLPSIPVI 36
Db      703 LKFAVLMMLLTYVGALFNGLLTLILMAVVSMTFLPVV 738

RESULT 8
US-09-949-016-6998
; Sequence 6998, Application US/09949016
; Patent No. 6812339
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Tue Feb 21 15:13:27 2006

us-09-830-972a-2_copy_1090_1125.ra1

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6998
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6998

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Best Local Similarity 72.2%; Pred. No. 3.2e-11;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

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Db

RESULT 9
US-09-270-767-45132
; Sequence 45132, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45132

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Db

RESULT 10
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; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
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; EARLIER APPLICATION NUMBER: 60/047,503
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313

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us-09-830-972a-2_copy_1090_1125.ra1

Tue Feb 21 15:13:27 2006

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 74.9%; Score 131; DB 2; Length 168;
Best Local Similarity 63.9%; Pred. No. 1.7e-09;
Matches 23; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKFAVLMVFTYVGVNGTLTLLALISLFSIPVI 36
DB 93 LKLA VFMWLTYYGVNGITLLILAE LLI FSVP IV 128

RESULT 12
US-09-949-016-8859
Sequence 8859, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8859
LENGTH: 192
TYPE: PRT
ORGANISM: Human
US-09-949-016-8859

Query Match 74.9%; Score 131; DB 2; Length 192;
Best Local Similarity 63.9%; Pred. No. 2e-09;
Matches 23; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 LKFAVLMVFTYVGVNGTLTLLALISLFSIPVI 36

DB 118 LKLA VFMWLTYYGVNGITLLILAE LLI FSVP IV 153

RESULT 13
US-08-700-607-3
Sequence 5, Application US/08700607
Patent No. 5856708
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,607
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0114 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: TFF1NOB01
CLONE: 31870
US-08-700-607-3

Query Match 70.9%; Score 124; DB 1; Length 241;
Best Local Similarity 61.1%; Pred. No. 2e-08;
Matches 22; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LKFAVLMVFTYVGVNGITLLILAE LLI FSVP IV 36
DB 162 LKLA VFMWLTYYGVNGITLLILAE LLI FSVP IV 197

RESULT 14
US-09-949-016-7290
Sequence 7290, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7290
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7290

Query Match      68.6%; Score 120; DB 2; Length 588;
Best Local Similarity 61.1%; Pred. No. 1.7e-07;
Matches 22; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY      1 LKFAVLMMVFTVVGALFNGTLTLLILALISLFSIPVI 36
      |||:::|||||:::|||||:::|||||:::
Db      502 LKALLFVILTFVGAIFNGTLTLLILGVLFTIPLL 537

RESULT 15
US-09-489-039A-12517
; Sequence 12517, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27/117,747
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12517
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12517

Query Match      35.1%; Score 61.5; DB 2; Length 242;
Best Local Similarity 44.7%; Pred. No. 2.2;
Matches 17; Conservative 4; Mismatches 8; Indels 9; Gaps 2;

QY      6 LMWV--FTYVGALP-----NGLTLLILALISLFSIP 34
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      188 LMVLLFTYAGYLGDLFVVOENLKLLIVAIIVLSVLP 225

Search completed: February 17, 2006, 03:58:22
Job time : 39.2222 secs
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us-09-830-972a-2_copy_1090_1125.rapbm

Tue Feb 21 15:13:28 2006

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; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-810-653-21

Query Match          100.0%; Score 175; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 126 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 161

RESULT 3
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US2002007493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

Query Match          100.0%; Score 175; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 287 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 322

RESULT 4
US-10-810-653-20
; Sequence 20, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

Query Match          100.0%; Score 175; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 287 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 322

RESULT 5
US-10-205-194-164
; Sequence 164, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Footcen-m2 reticulon
US-10-205-194-164

Query Match          100.0%; Score 175; DB 4; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
Db 306 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 341

RESULT 6
US-10-810-653-20
; Sequence 20, Application US/10810653
; Publication No. US20040253218A1
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us-09-830-972a-2_copy_1090_1125.rapbm

Tue Feb 21 15:13:28 2006

US-10-633-423-10
 ; Sequence 10, Application US/10633423
 ; Publication No. US20040191240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tohyama, Masaya
 ; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
 ; FILE REFERENCE: 59150-8023.US00
 ; CURRENT APPLICATION NUMBER: US/10/633,423
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: US 10/427,741
 ; PRIOR FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: JP 2003-92923
 ; PRIOR FILING DATE: 2003-03-28
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 1162
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-633-423-10

Query Match 100.0%; Score 175; DB 4; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 9.7e-14; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 |||||
 Db 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124

RESULT 7
 US-10-427-741-10
 ; Sequence 10, Application US/10427741
 ; Publication No. US20040191291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tohyama, Masaya
 ; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
 ; FILE REFERENCE: 59150-8023
 ; CURRENT APPLICATION NUMBER: US/10/427,741
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: JP 2003-92923
 ; PRIOR FILING DATE: 2003-03-28
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 1162
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-427-741-10

Query Match 100.0%; Score 175; DB 4; Length 1162;
 Best Local Similarity 100.0%; Pred. No. 9.7e-14; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 |||||
 Db 1089 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1124

RESULT 8
 US-09-893-348-18
 ; Sequence 18, Application US/09893348
 ; Patent No. US20020072493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal
 ; APPLICANT: COHEN, Irun R.
 ; APPLICANT: BESERMAN, Pierre
 ; APPLICANT: MOSONEGO, Alon
 ; APPLICANT: MOALEM, Gila
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
 ; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/314,161
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: US 09/218,277
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: FC1/US98/14715
 ; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: IL 124500
 ; PRIOR FILING DATE: 1998-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 1163
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-893-348-18

Query Match 100.0%; Score 175; DB 3; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 9.7e-14; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 |||||
 Db 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 9
 US-10-267-502-431
 ; Sequence 431, Application US/10267502
 ; Publication No. US20040071700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kim, Jaeseob
 ; APPLICANT: Galant, Ron
 ; TITLE OF INVENTION: Obesity Linked Genes
 ; FILE REFERENCE: LSD-07415
 ; CURRENT APPLICATION NUMBER: US/10/267,502
 ; CURRENT FILING DATE: 2003-01-27
 ; NUMBER OF SEQ ID NOS: 439
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 431
 ; LENGTH: 1163
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-267-502-431

Query Match 100.0%; Score 175; DB 4; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 9.7e-14; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
 |||||
 Db 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 10
 US-10-810-653-18
 ; Sequence 18, Application US/10810653
 ; Publication No. US20040253218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EISENBACH-SCHWARTZ, Michal
 ; APPLICANT: COHEN, Irun R.
 ; APPLICANT: BESERMAN, Pierre
 ; APPLICANT: MOSONEGO, Alon
 ; APPLICANT: MOALEM, Gila
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USE
 ; FILE REFERENCE: EIS-SCHWARTZ=2A
 ; CURRENT APPLICATION NUMBER: US/10/810,653
 ; CURRENT FILING DATE: 2004-03-29
 ; PRIOR APPLICATION NUMBER: US/09/893,348
 ; PRIOR FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/314,161
 ; PRIOR FILING DATE: 1999-05-19

```
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-810-653-18
```

```
Query Match 100.0%; Score 175; DB 5; Length 1163;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
|||||
Db 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125
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RESULT 11

```
US-11-111-953-184
; Sequence 184, Application US/11111953
; Publication No. US20050214844A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
```

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; TITLE OF INVENTION: 86 Human Secreted Proteins
; FILE REFERENCE: P2008PIC2
; CURRENT APPLICATION NUMBER: US/11/111,953
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: 10/219,793
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 09/209,462
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/12125
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/049,547
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,548
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,549
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,550
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,566
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,606
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,607
; PRIOR FILING DATE: 1997-06-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 737
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 184
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals stop translation
; US-11-111-953-184
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Query Match 99.4%; Score 174; DB 6; Length 175;
Best Local Similarity 97.2%; Pred. No. 1.9e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
|||||
Db 101 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 136
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RESULT 12

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US-09-893-348-25
; Sequence 25, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: CHEN, Irui R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSCONGO, Alon
; APPLICANT: MOALEM, Gile
```

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; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-893-348-25
```

```
Query Match 99.4%; Score 174; DB 3; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
|||||
Db 126 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 161
```

RESULT 13

```
US-09-978-360A-467
; Sequence 467, Application US/09978360A
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueret-Lydie
; APPLICANT: Robert, Severin
; APPLICANT: Cluaret, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIF
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
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; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 467
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -42..-1
US-09-978-360A-467

Query Match          99.4%; Score 174; DB 3; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.2e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSIPVI 36
    |||||
DB 126 LKPAVLMMVFTYVGVGALFNGLTLLILALISLFSVPVI 161

RESULT 14
US-10-660-946-1
; Sequence 1, Application US/10660946
; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/660,946
; FILING DATE: 12-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,213A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/700,607
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-660-946-1

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:58:38 ; Search time 11.5556 Seconds
(without alignments)
44.284 Million cell updates/sec

Title: US-09-830-972A-2_COPY_1090_1125
Perfect score: 175
Sequence: 1 LKPAVLMMVFTYVGVGLFGLTLILALISLFSIPVI 36

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	175	100.0	186	7 US-11-044-899-25	Sequence 25, Appl
2	175	100.0	1163	7 US-11-044-899-2	Sequence 2, Appl
3	175	100.0	1163	7 US-11-044-899-30	Sequence 30, Appl
4	174	99.4	186	7 US-11-044-899-24	Sequence 24, Appl
5	174	99.4	199	5 US-09-378-360A-167	Sequence 467, App
6	174	99.4	414	6 US-10-821-234-1170	Sequence 1170, Ap
7	174	99.4	1178	7 US-11-044-899-29	Sequence 29, Appl
8	152	86.9	186	7 US-11-044-899-23	Sequence 23, Appl
9	150	85.7	186	7 US-11-044-899-21	Sequence 21, Appl
10	150	85.7	186	7 US-11-044-899-22	Sequence 22, Appl
11	97	55.4	194	7 US-11-044-899-26	Sequence 26, Appl
12	63	36.0	150	7 US-11-044-899-27	Sequence 27, Appl
13	53	30.3	778	6 US-10-505-263-81	Sequence 81, Appl
14	51.5	29.4	769	6 US-10-505-263-81	Sequence 81, Appl
15	50	28.6	252	6 US-10-055-877-107	Sequence 107, App
16	50	28.6	276	6 US-10-055-877-111	Sequence 111, App
17	50	28.6	276	6 US-10-055-877-115	Sequence 115, App
18	50	28.6	355	7 US-11-218-281-26	Sequence 26, Appl
19	50	28.6	552	6 US-10-055-877-305	Sequence 305, App
20	50	28.6	664	6 US-10-624-932-10	Sequence 10, Appl
21	50	28.6	684	6 US-10-055-877-105	Sequence 105, App
22	50	28.6	704	6 US-10-055-877-113	Sequence 113, App
23	50	28.6	743	6 US-10-055-877-109	Sequence 109, App
24	49	28.0	400	7 US-11-229-371-123	Sequence 123, App
25	49	28.0	400	7 US-11-228-923-123	Sequence 123, App

26	49	28.0	424	7 US-11-229-371-113	Sequence 113, App
27	49	28.0	424	7 US-11-228-923-113	Sequence 113, App
28	49	28.0	664	6 US-10-055-877-306	Sequence 306, App
29	49	28.0	664	6 US-10-055-877-307	Sequence 307, App
30	47.5	27.1	315	7 US-11-044-347B-2	Sequence 2, Appl
31	47.5	27.1	395	7 US-11-073-176-188	Sequence 188, App
32	47.5	27.1	4473	6 US-10-895-064-460	Sequence 460, App
33	47	26.9	319	6 US-10-873-528-144	Sequence 64, Appl
34	47	26.9	431	6 US-10-793-626-566	Sequence 2566, AD
35	46.5	26.6	181	6 US-10-793-626-1842	Sequence 1842, AD
36	46.5	26.6	288	7 US-11-098-686-10850	Sequence 10850, A
37	46.5	26.6	530	6 US-10-055-877-316	Sequence 316, App
38	46	26.3	229	6 US-10-873-528-131	Sequence 131, App
39	46	26.3	341	7 US-11-082-389-18	Sequence 18, Appl
40	46	26.3	407	7 US-11-166-412-57	Sequence 57, Appl
41	46	26.3	529	7 US-11-166-412-58	Sequence 58, Appl
42	46	26.3	546	7 US-11-166-412-59	Sequence 59, Appl
43	45.5	26.0	196	6 US-10-793-626-2584	Sequence 2584, Ap
44	45.5	26.0	336	6 US-10-793-626-1858	Sequence 1858, Ap
45	45.5	26.0	337	6 US-10-793-626-444	Sequence 444, App

ALIGNMENTS

RESULT 1
US-11-044-899-25
; Sequence 25, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044, 899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830, 972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107, 446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-25
Query Match 100.0%; Score 175; DB 7; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKPAVLMMVFTYVGVGLFGLTLILALISLFSIPVI 36
Db 113 LKPAVLMMVFTYVGVGLFGLTLILALISLFSIPVI 148
RESULT 2
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044, 899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830, 972

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; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2
Query Match      100.0%; Score 175; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
   |||||
Db 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 3
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US/11/044,899
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE: VARIANT
; LOCATION: (1) (1163) at all Xaa position
; OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30
Query Match      100.0%; Score 175; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
   |||||
Db 1090 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 1125

RESULT 4
US-11-044-899-24
; Sequence 24, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US/11/044,899
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-24
Query Match      99.4%; Score 174; DB 5; Length 1163;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKFAVLMMVFTYVGALFNGLTLLILALISLFSIPVI 36
   |||||
Db 113 LKFAVLMMVFTYVGALFNGLTLLILALISLFSVPVI 148

RESULT 5
US-09-978-360A-467
; Sequence 467, Application US/0978360A
; Publication No. US20060009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Ducloer, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Jober, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.USA.CIP
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US/09/978,360A
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/IB98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 467
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -42...-1
US-09-978-360A-467
Query Match      99.4%; Score 174; DB 5; Length 199;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVI 36
 DB 126 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVI 161

RESULT 6
 US-10-821-234-1170
 ; Sequence 1170, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: Pt_SEQ_Genes Version 1.0
 ; SEQ ID NO 1170
 ; LENGTH: 414
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1170

Query Match 99.4%; Score 174; DB 6; Length 414;
 Best Local Similarity 97.2%; Pred. No. 5e-15; Indels 0; Gaps 0;
 Matches 35; Conservative 1; Mismatches 0;

QY 1 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVI 36
 DB 341 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVI 376

RESULT 7
 US-11-044-899-29
 ; Sequence 29, Application US/11044899
 ; Publication No. US20050260616A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwab, M.
 ; APPLICANT: Chen, M.
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
 ; FILE REFERENCE: 10200-017-999
 ; CURRENT APPLICATION NUMBER: US/11/044,899
 ; CURRENT FILING DATE: 2005-01-26
 ; PRIOR APPLICATION NUMBER: 09/830,972
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: PCT/US99/26160
 ; PRIOR FILING DATE: 1999-11-05
 ; PRIOR APPLICATION NUMBER: 60/107,446
 ; PRIOR FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 1178
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(1178) at all Xaa position
 ; OTHER INFORMATION: Xaa = any amino acid
 US-11-044-899-29

Query Match 99.4%; Score 174; DB 7; Length 1178;
 Best Local Similarity 97.2%; Pred. No. 1.4e-14; Indels 0; Gaps 0;
 Matches 35; Conservative 1; Mismatches 0;

QY 1 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVI 36
 DB 113 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVI 148

DB 1105 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVI 1140

RESULT 8
 US-11-044-899-23
 ; Sequence 23, Application US/11044899
 ; Publication No. US20050260616A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwab, M.
 ; APPLICANT: Chen, M.
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
 ; FILE REFERENCE: 10200-017-999
 ; CURRENT APPLICATION NUMBER: US/11/044,899
 ; CURRENT FILING DATE: 2005-01-26
 ; PRIOR APPLICATION NUMBER: 09/830,972
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: PCT/US99/26160
 ; PRIOR FILING DATE: 1999-11-05
 ; PRIOR APPLICATION NUMBER: 60/107,446
 ; PRIOR FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Gallus gallus
 US-11-044-899-23

Query Match 86.9%; Score 152; DB 7; Length 186;
 Best Local Similarity 75.0%; Pred. No. 1.4e-12; Indels 1; Gaps 0;
 Matches 27; Conservative 8; Mismatches 1;

QY 1 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVI 36
 DB 113 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVI 148

RESULT 9
 US-11-044-899-21
 ; Sequence 21, Application US/11044899
 ; Publication No. US20050260616A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwab, M.
 ; APPLICANT: Chen, M.
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
 ; FILE REFERENCE: 10200-017-999
 ; CURRENT APPLICATION NUMBER: US/11/044,899
 ; CURRENT FILING DATE: 2005-01-26
 ; PRIOR APPLICATION NUMBER: 09/830,972
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: PCT/US99/26160
 ; PRIOR FILING DATE: 1999-11-05
 ; PRIOR APPLICATION NUMBER: 60/107,446
 ; PRIOR FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-044-899-21

Query Match 85.7%; Score 150; DB 7; Length 186;
 Best Local Similarity 72.2%; Pred. No. 2.4e-12; Indels 1; Gaps 0;
 Matches 26; Conservative 9; Mismatches 1;

QY 1 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVI 36
 DB 113 LKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVI 148

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RESULT 10
US-11-044-899-22
; Sequence 22, Application US/11044899
; Publication NO. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-22

Query Match      85.7%; Score 150; DB 7; Length 186;
Best Local Similarity 72.2%; Pred. No. 2.4e-12;
Matches 26; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
Db      113 LKFAVLMWLTYYVGALFNGLTLLILMAVSMFTLPV 148

RESULT 11
US-11-044-899-26
; Sequence 26, Application US/11044899
; Publication NO. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 194
; TYPE: PRT
; ORGANISM: C. elegans
US-11-044-899-26

Query Match      55.4%; Score 97; DB 7; Length 194;
Best Local Similarity 41.7%; Pred. No. 1.2e-05;
Matches 15; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy      1 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 36
Db      113 IKFGLVLSLTIIASWFSGFTLILGLLVFSVPKV 148

RESULT 12
US-11-044-899-27
; Sequence 27, Application US/11044899
; Publication NO. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 150
; TYPE: PRT
; ORGANISM: D. melanogaster
US-11-044-899-27

Query Match      36.0%; Score 63; DB 7; Length 150;
Best Local Similarity 51.9%; Pred. No. 0.18;
Matches 14; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy      1 LKFAVLMWVFTYVGALFNGLTLLILAL 27
Db      114 LKFLVLLCGINLIGDCFNGLTLLIFGM 140

RESULT 13
US-10-505-263-83
; Sequence 83, Application US/10505263
; Publication NO. US20060014940A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Case Western Reserve University
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Mount, David B
; APPLICANT: Romero, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
; FILE REFERENCE: 1242/50/2 PCT/US
; CURRENT APPLICATION NUMBER: US/10/505,263
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/360,275
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US03/06469
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 83
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-505-263-83

Query Match      30.3%; Score 53; DB 6; Length 769;
Best Local Similarity 44.0%; Pred. No. 16;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy      2 KFAVLMWVFTYVGALFNGLTLLILA 26
Db      460 RWDVIVWFTCVSAIILGLDLGLLA 484

RESULT 14
US-10-505-263-81
; Sequence 81, Application US/10505263
; Publication NO. US20060014940A1
; GENERAL INFORMATION:
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us-09-830-972a-2_copy_1090_1125.rapbn

Tue Feb 21 15:13:28 2006

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; APPLICANT: Vanderbilt University
; APPLICANT: Case Western Reserve University
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Mount, David B
; APPLICANT: Romero, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
; FILE REFERENCE: 1242/50/2 PCT/US
; CURRENT APPLICATION NUMBER: US/10/505,263
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/360,275
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US03/06469
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Xenopus laevis
; US-10-505-263-81

Query Match      29.4%; Score 51.5; DB 6; Length 778;
Best Local Similarity 37.1%; Pred. No.25;
Matches 13; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 2 KFAVLMMVFTYVGVGALFNGTLTLLILALISLPSIPVI 36
DB 471 KMDSVIWMVFTCIASILLGLDGLLGL-LFGLVTI 504

RESULT 15
US-10-055-877-107
; Sequence 107, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eichen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shanket, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23

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; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-055-877-107

Query Match      28.6%; Score 50; DB 6; Length 252;
Best Local Similarity 30.8%; Pred. No.13;
Matches 8; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 10 FTVGVGALFNGTLTLLILALISLPSIPV 35
DB 101 YLYVAILLCGLTAIVIVIVSLCTPI 126

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Job time : 12.5556 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
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(without alignments)
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Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 EPEDEDEDEDEDEDEDELEVL 27
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	139	100.0	360	3	US-09-893-348-20 Sequence 20, Appl
2	139	100.0	360	5	US-10-810-653-20 Sequence 20, Appl
3	139	100.0	379	4	US-10-205-194-164 Sequence 164, Appl
4	139	100.0	1163	3	US-09-893-348-18 Sequence 18, Appl
5	139	100.0	1163	5	US-10-810-653-18 Sequence 18, Appl
6	119.5	86.0	1162	4	US-10-633-423-10 Sequence 10, Appl
7	119.5	86.0	1162	4	US-10-427-741-10 Sequence 10, Appl
8	119.5	86.0	1163	4	US-10-267-502-431 Sequence 431, Appl
9	111.5	80.2	373	3	US-09-789-386-6 Sequence 6, Appl
10	111.5	80.2	373	3	US-09-789-386-6 Sequence 6, Appl
11	111.5	80.2	373	3	US-09-893-348-20 Sequence 20, Appl
12	111.5	80.2	373	4	US-10-060-036-72 Sequence 72, Appl
13	111.5	80.2	373	4	US-10-408-967-8 Sequence 8, Appl
14	111.5	80.2	373	4	US-10-466-258-4 Sequence 4, Appl
15	111.5	80.2	373	4	US-10-466-391A-4 Sequence 4, Appl
16	111.5	80.2	373	5	US-10-810-653-24 Sequence 24, Appl
17	111.5	80.2	373	5	US-10-347-669-6 Sequence 6, Appl
18	111.5	80.2	1192	3	US-09-789-386-2 Sequence 2, Appl
19	111.5	80.2	1192	3	US-09-758-140-6 Sequence 6, Appl
20	111.5	80.2	1192	3	US-09-893-348-23 Sequence 23, Appl
21	111.5	80.2	1192	3	US-09-972-599A-6 Sequence 6, Appl
22	111.5	80.2	1192	4	US-10-060-036-71 Sequence 71, Appl
23	111.5	80.2	1192	4	US-10-408-967-7 Sequence 7, Appl
24	111.5	80.2	1192	4	US-10-267-502-429 Sequence 429, Appl
25	111.5	80.2	1192	4	US-10-327-213-9 Sequence 9, Appl
26	111.5	80.2	1192	4	US-10-466-258-9 Sequence 9, Appl
27	111.5	80.2	1192	4	US-10-466-391A-9 Sequence 9, Appl

28	111.5	80.2	1192	5	US-10-810-653-23 Sequence 23, Appl
29	111.5	80.2	1192	6	US-11-090-836-3 Sequence 3, Appl
30	111.5	80.2	1192	6	US-11-090-846-3 Sequence 3, Appl
31	111.5	80.2	1192	6	US-11-090-847-3 Sequence 3, Appl
32	99.5	71.6	306	4	US-10-437-155-242884 Sequence 197583
33	97	69.8	51	4	US-10-423-155-242884 Sequence 242884
34	97	69.8	208	3	US-09-214-861A-2 Sequence 2, Appl
35	97	69.8	208	5	US-10-728-195-2 Sequence 2, Appl
36	97	69.8	209	4	US-10-147-447-3 Sequence 3, Appl
37	97	69.8	209	4	US-10-300-072-3 Sequence 3, Appl
38	97	69.8	209	4	US-10-170-385-385 Sequence 385, Appl
39	97	69.8	209	4	US-10-456-949-3 Sequence 3, Appl
40	97	69.8	209	4	US-10-456-947-3 Sequence 3, Appl
41	97	69.8	209	4	US-10-718-495-3 Sequence 3, Appl
42	97	69.8	209	4	US-10-717-984-3 Sequence 3, Appl
43	97	69.8	209	5	US-10-733-878-493 Sequence 493, Appl
44	97	69.8	209	5	US-10-938-992-54 Sequence 54, Appl
45	97	69.8	244	4	US-10-264-049-3144 Sequence 3144, Appl

ALIGNMENTS

RESULT 1
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSNEGO, Alon
; APPLICANT: MOSNEGO, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ#21
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

Query Match 100.0%; Score 139; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDEDELEVL 57

RESULT 2
US-10-810-653-20
; Sequence 20, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSNEGO, Alon
; APPLICANT: MOSNEGO, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

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; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-810-653-20

Query Match      100.0%; Score 139; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDELEVL 57

RESULT 3
US-10-205-194-164
; Sequence 164, Application US/10205194
; Publication No. US2003013430A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Allstair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foccen-m2 reticulon
US-10-205-194-164

Query Match      100.0%; Score 139; DB 4; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDELEVL 57

RESULT 4
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESSEMAN, Pierre
```

```
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOLEW, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match      100.0%; Score 139; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDELEVL 57

RESULT 5
US-10-810-653-18
; Sequence 18, Application US/10810653
; Publication No. US20040253218A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESSEMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOLEW, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ-2A
; CURRENT APPLICATION NUMBER: US/10/810,653
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/893,348
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-810-653-18

Query Match      100.0%; Score 139; DB 5; Length 1163;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDELEVL 57

RESULT 6
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESSEMAN, Pierre
```

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US-10-633-423-10
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023-US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-633-423-10
Query Match      86.0%; Score 119.5; DB 4; Length 1162;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPDEDEDEDEE-EEDEDEDELEVL 56

RESULT 7
US-10-427-741-10
; Sequence 10, Application US/10427741
; Publication No. US20040191291A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023
; CURRENT APPLICATION NUMBER: US/10/427,741
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: JP 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-427-741-10
Query Match      86.0%; Score 119.5; DB 4; Length 1162;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPDEDEDEDEE-EEDEDEDELEVL 56

RESULT 8
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
US-10-267-502-431
; Sequence 10, Application US/10633423
; Publication No. US20040191240A1
; GENERAL INFORMATION:
; APPLICANT: Tohyama, Masaya
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR NERVE REGENERATION
; FILE REFERENCE: 59150-8023-US00
; CURRENT APPLICATION NUMBER: US/10/633,423
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 10/427,741
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 2003-92923
; PRIOR FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431
Query Match      86.0%; Score 119.5; DB 4; Length 1163;
Best Local Similarity 92.6%; Pred. No. 0.00061;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPDEDEDEDEE-EEDEDEDELEVL 56

RESULT 9
US-09-789-386-6
; Sequence 6, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
Query Match      80.2%; Score 111.5; DB 3; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
Db 30 EPDEDEE-EEDEDEDEDEDELEVL 55

RESULT 10
US-09-765-205-6
; Sequence 6, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6
Query Match      80.2%; Score 111.5; DB 3; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
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; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-391A-4

Query Match      80.2%; Score 111.5; DB 4; Length 373;
Best Local Similarity 85.2%; Pred. No. 0.0013;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY      1 EPEDDEDEDEDEDEDEDEDELEVL 27
        ||||| ||||| :|||
Db      30 EPEDDE-EEEEDEDEDELEVL 55

Search completed: February 17, 2006, 04:03:20
Job time : 97.6667 secs
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degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Kinobymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of CNS neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient e.g. where anti-neurotrophic cytokines are secreted or test molecules which can antagonise cytokine receptors are used to treat or prevent disorders of the CNS. The present sequence is a fragment of rat Nogo-A protein shown in AAV7110, which is used in the construction of mutant Nig. The mutant is composed of His-tag/Tag/vector/Nogo-A sequence aa 1-171/vector. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV7110. SEQ ID numbers 35-42 are referred to in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers

sequence 171 AA:

PI Schwab ME, Chen MS;
XX WPT; 2000-400052/34.
XX
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Example; Page; 122pp; English.
XX
XX The patent relates to neurite growth inhibitor Nogo which is free of all
XX central nervous system (CNS) myelin material with which it is natively
XX associated. Nogo proteins and fragments displaying neurite growth
XX inhibitory activity are used in the treatment of neoplastic disease of
XX the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
XX ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
XX oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and
XX degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
XX Therapeutics which promote Nogo activity can be used to treat or prevent
XX hyperproliferative or benign dysplastic disorders e.g. psoriasis
XX and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
XX used to inhibit production of Nogo protein to induce regeneration of
XX neurons or to promote structural plasticity of the CNS in disorders where
XX neurite growth, regeneration or maintenance are deficient or desired. The
XX animal models can be used in diagnostic and screening methods for
XX treatment or prevention of disorders and to screen for or test molecules which can
XX treat or prevent disorders or diseases of the CNS. The present sequence
XX is derived by fusing two fragments of rat Nogo A protein shown in
XX AA7V1310. The fragment is used in the construction of mutant Nogo-B. The
XX mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +
XX 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
XX sites of Nogo protein. Major inhibitory region was identified in the Nogo
XX A sequence from amino acids 172-974, particularly amino acids 542-722. In
XX addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
XX fibroblast spreading. Note: The present sequence is not given in the
XX specification but is derived from rat Nogo A sequence shown in AA7V1310.
XX SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
XX disclosure of the specification. However, the specification does not
XX include sequences for these SEQ ID numbers

CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (IgA- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-B, an example of NS-specific
CC antigen
XX
SQ Sequence 360 AA;

Query Match 100.0%; Score 139; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDEDEDELEVL 57

RESULT 5
AAV71385
ID AAV71385 standard; protein; 361 AA.
AC AAV71385;
XX
DT 02-NOV-2000 (first entry)
DE
DE Alternative version of rat neurite growth inhibitor Nogo B.
KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX
XX Location/Qualifiers
FH Key
FH Region
FT 1..172
FT /note= "Corresponds to amino acids 1-172 of Nogo A
FT protein shown in AAV71310"
FT Inhibitory-site 1..171
FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31..58
FT /note= "Acidic region"
FT Region 173..361
FT /note= "Corresponds to amino acids 975-1163 of Nogo A
FT protein (AAV71310)"
FT Region 174..361
FT /note= "This region is common to Nogo A, B and C
FT isoforms"
FT Domain 186..221
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 222
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 269..271
FT /note= "Asn is N-glycosylated"
FT Modified-site 271
FT /note= "Protein kinase C (PKC) site"

FT Modified-site 287
FT /note= "Protein kinase C (PKC) site"
FT Domain 288..323
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 339..341
FT /note= "Asn is N-glycosylated"
FT Modified-site 341
FT /note= "Protein kinase C (PKC) site"
PN WO200031235-A2.
PD 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX 06-NOV-1998; 98US-0107446P.
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX Schwab ME, Chen MS;
XX WPI; 2000-400052/34.
DR Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 4; Page; 122pp; English.
XX
XX The present sequence is an alternative version of rat Nogo B protein
XX which is a potent neural cell growth inhibitor and is free of all central
XX nervous system (CNS) myelin material with which it is native
XX associated. The Nogo B transcript arises as a result of alternative
XX splicing of Nogo gene. Nogo protein and fragments displaying neurite
XX growth inhibitory activity are used in the treatment of neoplastic
XX disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
XX craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
XX neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma
XX and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
XX diseases. Therapeutics which promote Nogo activity can be used to treat
XX or prevent hyperproliferative or benign dysproliferative disorders e.g.
XX psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
XX acids can be used to inhibit production of Nogo protein to induce
XX regeneration of neurons or to promote structural plasticity of the CNS in
XX disorders where neurite growth, regeneration or maintenance are deficient
XX or desired. The animal models can be used in diagnostic and screening
XX methods for predisposition to disorders and to screen for or test
XX molecules which can treat or prevent disorders or diseases of the CNS.
XX Note: The present sequence is not given in the specification but is
XX derived from Nogo A protein sequence (AAV71310) and corresponds to
XX residues 1-172 fused to 975-1163 of Nogo A. This sequence is an
XX alternative version of the Nogo B sequence (see AAV71383) described in
XX the specification as being residues 1-172 fused to C-terminal 188 amino
XX acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
XX claim 32 and SEQ ID NO: 29 in disclosure of the specification. However
XX the specification does not include sequences for these SEQ ID numbers
XX
SQ Sequence 361 AA;

Query Match 100.0%; Score 139; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDEDEDEDELEVL 57

RESULT 6
ADB85283
ID ADB85283 standard; protein; 379 AA.
XX

XX	AAV71557;	
AC	02-NOV-2000 (first entry)	
XX	Rat Nogo A truncated protein used in the construction of mutant Nogo-A.	
XX	Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;	
XX	central nervous system; neoplastic disease; antiproliferative; glioma;	
KW	antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;	
KW	degenerative nerve disease; Alzheimer's disease; Parkinson's disease;	
KW	hyperproliferative disorder; benign dysproliferative disorder; diagnosis;	
KW	psoriasis; tissue hypertrophy; neuronal regeneration; treatment;	
KW	structural plasticity; screening; mutant; mutein.	
OS	Rattus sp.	
XX	W02000031235-A2.	
XX	02-JUN-2000.	
XX	05-NOV-1999; 99WO-US026160.	
XX	06-NOV-1998; 98US-0107446P.	
XX	(SCHW/) SCHWAB M E.	
PA	(CHEN/) CHEN M S.	
XX	Schwab ME, Chen MS;	
XX	WPI; 2000-400052/34.	
XX	Nogo proteins and nucleic acids useful for treating neoplastic disorders	
XX	of the central nervous system and inducing regeneration of neurons.	
XX	Example; Page; 122pp; English.	
XX	The patent relates to neurite growth inhibitor Nogo which is free of all	
CC	central nervous system (CNS) myelin material with which it is natively	
CC	associated. Nogo proteins and fragments displaying neurite growth	
CC	inhibitory activity are used in the treatment of neoplastic disease of	
CC	the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,	
CC	ependymoma, pinealoma, haemangioblastoma, acoustic neuroma and	
CC	oligodendroglioma, menigioma, neuroblastoma or retinoblastoma and	
CC	degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.	
CC	Therapeutics which promote Nogo activity can be used to treat or prevent	
CC	hyperproliferative or benign dysproliferative disorders e.g. psoriasis	
CC	and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can	
CC	used to inhibit production of Nogo protein to induce regeneration of	
CC	neurons or to promote structural plasticity of the CNS in disorders where	
CC	neurite growth, regeneration or maintenance are deficient or desired. The	
CC	animal models can be used in diagnostic and screening methods for	
CC	treat or prevent disorders and to screen for or test molecules which can	
CC	readjust or prevent disorders or diseases of the CNS. The present sequence	
CC	is a truncated form of rat Nogo A protein shown in AAV71310, which is	
CC	used in the construction of mutant Nogo-A. Nogo-A is composed of His-	
CC	tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were	
CC	used for mapping the inhibitory sites of Nogo protein. Major inhibitory	
CC	region was identified in the Nogo A sequence from amino acids 172-974,	
CC	particularly amino acids 542-722. In addition, N-terminal region 1-171	
CC	was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The	
CC	present sequence is not given in the specification but is derived from	
CC	rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred	
CC	in claim 32 and SEQ ID NO: 29 in disclosure of the specification.	
CC	However, the specification does not include sequences for these SEQ ID	
CC	numbers	
XX	Sequence 1162 AA;	
XX	Query Match 100.0%; Score 139; DB 3; Length 1162;	
XX	Best Local Similarity 100.0%; Pred. No. 9.7e-07;	
XX	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY	1	EFDEDEDEDEDEDEDEDEDELEVL	27
DB	31	EFDEDEDEDEDEDEDEDEDELEVL	57
RESULT	9		
AAV71310			
ID	AAV71310 standard; protein; 1163 AA.		
XX	AAV71310;		
AC	02-NOV-2000 (first entry)		
XX	Rat neurite growth inhibitor Nogo A.		
XX	Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;		
KW	central nervous system; neoplastic disease; antiproliferative; glioma;		
KW	antisense gene therapy; neuroblastoma; menigioma; retinoblastoma;		
KW	degenerative nerve disease; Alzheimer's disease; Parkinson's disease;		
KW	hyperproliferative disorder; benign dysproliferative disorder; diagnosis;		
KW	psoriasis; tissue hypertrophy; neuronal regeneration; treatment;		
KW	structural plasticity; screening.		
OS	Rattus sp.		
XX			
XX	Key Location/Qualifiers		
FT	Inhibitory-site 1..171		
FT	/note="Inhibits NIH 3T3 fibroblast spreading"		
FT	Modified-site 30		
FT	/note="Casein kinase II site"		
FT	Region 31..58		
FT	/note="Acidic region"		
FT	Region 31..57		
FT	/note="Region specifically described in claim 16"		
FT	Region 172..259		
FT	/note="This region is not essential for inhibitory activity"		
FT	Modified-site 233		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 242..244		
FT	/note="Asn is N-glycosylated"		
FT	Modified-site 291		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 295		
FT	/note="Protein kinase C (PKC) site"		
FT	Misc-difference 404		
FT	/note="Encoded by TGT"		
FT	Modified-site 436		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 468..470		
FT	/note="Asn is N-glycosylated"		
FT	Modified-site 484		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 488		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 502		
FT	/note="Casein kinase II site"		
FT	Inhibitory-site 542..722		
FT	Modified-site 576		
FT	/note="Casein kinase II site"		
FT	Peptide 623..640		
FT	/note="used as immunogen to generate antibody AS 472"		
FT	Modified-site 626		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 694..696		
FT	/note="Asn is N-glycosylated"		
FT	Modified-site 715		
FT	/note="Casein kinase II site"		
FT	Peptide 762..1163		
FT	/note="used as immunogen to generate antibody AS Bruna"		
FT	Modified-site 784		
FT	/note="Protein kinase C (PKC) site"		
FT	Modified-site 821		

FT /note= "Protein kinase C (PKC) site"
FT 850
FT /note= "Protein kinase C (PKC) site"
FT 855
FT /note= "Protein kinase C (PKC) site"
FT 863
FT /note= "Casein kinase II site"
FT 868
FT /note= "Protein kinase C (PKC) site"
FT 893
FT /note= "Protein kinase C (PKC) site"
FT 912. .914
FT /note= "Asn is N-glycosylated"
FT 925. .927
FT /note= "Asn is N-glycosylated"
FT 954
FT /note= "PKC and casein kinase II sites"
FT 956
FT /note= "PKC and casein kinase II sites"
FT 975. 1162
FT /note= "This region is not essential for inhibitory
FT activity"
FT 976. 1163
FT /note= "C-terminal common region found in Nogo A, B and C
FT isoforms"
FT 988. 1023
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region specifically
FT described in claim 16"
FT 1024
FT /note= "Protein kinase C (PKC) site"
FT 1071. 1073
FT /note= "Asn is N-glycosylated"
FT 1073
FT /note= "Protein kinase C (PKC) site"
FT 1089
FT /note= "Protein kinase C (PKC) site"
FT 1090. 1125
FT /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region specifically
FT described in claim 16"
FT 1141. 1143
FT /note= "Asn is N-glycosylated"
FT 1143
FT /note= "Protein kinase C (PKC) site"
FT
XX WO200031235-A2.
XX
XX 02-JUN-2000.
XX
XX 05-NOV-1999; 99WO-US026160.
XX
XX 06-NOV-1998; 98US-0107446P.
XX
XX (SCHW/) SCHWAB M E.
XX (CHEN/) CHEN M S.
XX
XX Schwab ME, Chen MS;
XX
XX WPI; 2000-400052/34.
XX N-PSDB; AAD01173.
XX
XX Nogo proteins and nucleic acids useful for treating neoplastic disorders
XX of the central nervous system and inducing regeneration of neurons.
XX
XX Claim 3; Fig 2A; 122pp; English.
XX
XX The present sequence is a rat Nogo A protein which is a potent neural
XX cell growth inhibitor and is free of all central nervous system (CNS)
XX myelin material with which it is natively associated. The protein was
XX derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated
XX from hexanucleotides-primed rat brain stem/spinal cord library, and Oll18
XX cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins

CC and fragments displaying neurite growth inhibitory activity are used in
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribosomes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
XX Sequence 1163 AA;
SQ
Query Match 100.0%; Score 139; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
DB 31 EPEDEDEDEDEDEDEDEDEDEDELEVL 57
RESULT 10
AAY71384
ID AAY71384 standard; protein; 1163 AA.
XX
XX AC AAY71384;
XX
XX 02-NOV-2000 (first entry)
XX
XX Alternative version of rat neurite growth inhibitor Nogo A.
XX
XX Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
XX central nervous system; neoplastic disease; antiproliferative; glioma;
XX antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
XX degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
XX hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
XX psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
XX structural plasticity; screening.
XX
XX Rattus sp.
XX
XX OS
XX
XX Key Location/Qualifiers
XX Inhibitory-site 1. .171
XX /note= "Inhibits NIH 3T3 fibroblast spreading"
XX Modified-site 30
XX /note= "Casein kinase II site"
XX Region 31. .58
XX /note= "Acidic region"
XX Region 172. .259
XX /note= "This region is not essential for inhibitory
XX activity"
XX Misc-difference 223
XX /label= Unknown
XX /note= "There is Leu at this position in the sequence
XX shown in AAY71310"
XX
XX Modified-site 233
XX /note= "Protein kinase C (PKC) site"
XX Modified-site 242. .244
XX /note= "Asn is N-glycosylated"
XX Modified-site 291
XX /note= "Protein kinase C (PKC) site"

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FT Modified-site 484 /note= "Protein kinase C (PKC) site"
FT Modified-site 488 /note= "Protein kinase C (PKC) site"
FT Modified-site 502 /note= "Casein kinase II site"
FT Inhibitory-site 542. .722
FT Modified-site 576 /note= "Casein kinase II site"
FT Peptide 623. .640
FT /note= "used as immunogen to generate antibody AS 472"
FT Modified-site 626 /note= "Protein kinase C (PKC) site"
FT Misc-difference 661 /note= "There is Asn at this position in the sequence
FT /shown= in AAY71310"
FT Modified-site 694. .696 /note= "Asn is N-glycosylated"
FT Modified-site 715 /note= "Casein kinase II site"
FT Peptide 762. .1163
FT Modified-site 784 /note= "used as immunogen to generate antibody AS Bruna"
FT Misc-difference 820 /note= "Protein kinase C (PKC) site"
FT /note= "There is Leu at this position in the sequence
FT /shown= in AAY71310"
FT Modified-site 821 /note= "Protein kinase C (PKC) site"
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FT Modified-site 855 /note= "Protein kinase C (PKC) site"
FT Modified-site 863 /note= "Protein kinase C (PKC) site"
FT Modified-site 868 /note= "Casein kinase II site"
FT Modified-site 893 /note= "Protein kinase C (PKC) site"
FT Modified-site 912. .914 /note= "Protein kinase C (PKC) site"
FT Modified-site 925. .927 /note= "Asn is N-glycosylated"
FT Modified-site 954 /note= "Asn is N-glycosylated"
FT Modified-site 956 /note= "PKC and casein kinase II sites"
FT Modified-site 975. .1162 /note= "PKC and casein kinase II sites"
FT Region /note= "This region is not essential for inhibitory
FT activity"
FT Region 976. .1163 /note= "C-terminal common region found in Nogo A, B and C
FT isoforms"
FT Domain 988. .1023 /label= Transmembrane domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 1024 /note= "Protein kinase C (PKC) site"
FT Modified-site 1071. .1073 /note= "Asn is N-glycosylated"
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FT Modified-site 1073 /note= "Protein kinase C (PKC) site"
FT Modified-site 1089 /note= "Protein kinase C (PKC) site"
FT Domain 1090. .1125 /label= Transmembrane domain
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FT Modified-site 1141. .1143 /note= "Asn is N-glycosylated"
FT Modified-site 1143 /note= "Protein kinase C (PKC) site"
FT XX WO200031235-A2.
FT XX 02-JUN-2000.
FT XX 05-NOV-1999; 99WO-US026160.
FT XX 06-NOV-1998; 98US-0107446P.
FT (SCHW/) SCHWAB M E.
FT (CHEN/) CHEN M S.
FT Schwab ME, Chen MS;
FT WPI; 2000-400052/34.
FT Nogo proteins and nucleic acids useful for treating neoplastic disorders
FT of the central nervous system and inducing regeneration of neurons.
FT Claim 3; Fig 13; 122pp; English.
FT The present sequence is an alternative version of rat Nogo A protein
FT which is a potent neural cell growth inhibitor and is free of all central
FT nervous system (CNS) myelin material with which it is natively
FT associated. Nogo proteins and fragments displaying neurite growth
FT inhibitory activity are used in the treatment of neoplastic disease of
FT the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
FT oligodendroglioma, haemangioblastoma, acoustic neuroma,
FT degenerative nerve diseases e.g. Alzheimer's and Parkinson's disease.
FT Therapeutics which promote Nogo activity can be used to treat or prevent
FT hyperproliferative or benign dysproliferative disorders e.g. psoriasis
FT and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
FT used to inhibit production of Nogo protein to induce regeneration of
FT neurons or to promote structural plasticity of the CNS in disorders where
FT neurite growth, regeneration or maintenance are deficient or desired. The
FT animal models can be used in diagnostic and screening methods for
FT predisposition to disorders and to screen for ot test molecules which can
FT treat or prevent disorders or diseases of the CNS. Note: The present
FT sequence is an alternative version of the Nogo A sequence shown in Fig.
FT 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
FT ID NO: 29 in disclosure of the specification. However the specification
FT does not include sequences for these SEQ ID numbers
FT XX
FT SQ Sequence 1163 AA;
FT Query Match 100.0%; Score 139; DB 3; Length 1163;
FT Best Local Similarity 100.0%; Pred. No. 9.7e-07;
FT Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT Qy 1 EPEDEDEDEDEDEDEDEDEDEDELELEVL 27
FT |||||
FT Db 31 EPEDEDEDEDEDEDEDEDEDEDELELEVL 57
FT
FT RESULT 11
FT ABB81074
FT ID ABB81074 standard; protein; 1163 AA.
FT XX
FT AC ABB81074;
FT XX
FT DT 05-NOV-2002 (first entry)
```

XX	Rat neurotransmitter receptor protein Nogo-A.	
DE		
XX	Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;	
KW	central nervous system; peripheral nervous system; tranquilizer; Nogo;	
KW	vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;	
KW	nutropic; antiparkinsonian; ophthalmological; analgesic; hepatocytic;	
KW	osteopathic; vasotropic; nephrologic; cytostatic; antigen; gene therapy;	
KW	neurotransmitter receptor; rat; receptor.	
XX		
OS	Rattus norvegicus.	
XX		
PN	US2002072493-A1.	
PN	13-JUN-2002.	
PD		
XX		
PF	28-JUN-2001; 2001US-00893348.	
PR	19-MAY-1998; 98IL-00124500.	
PR	21-JUL-1998; 98WO-US014715.	
PR	22-DEC-1998; 98US-00218277.	
PR	19-MAY-1999; 99US-00314161.	
XX	(YEDA) YEDA RES & DEV CO LTD.	
PA		
XX	Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;	
PI	Moalem G;	
PT		
DR	WPI. 2002-607255/65.	
DR	N-PSDB; AEN86600.	
XX		
PT	Promoting nerve regeneration and preventing neuronal degeneration in the	
PT	central/peripheral nervous system from injury/disease, comprises	
PT	administering nervous system-specific activated T cells/antigen, or	
PT	analogs/peptides.	
XX		
XX	Example 5; Page 44-47; 93pp: English.	
XX		
CC	The invention relates to promoting nerve regeneration or conferring	
CC	neuroprotection and preventing or inhibiting neuronal degeneration in the	
CC	central/peripheral nervous system (NS). The method involves administering	
CC	NS-specific activated T cells, NS-specific antigen, its analogue or its	
CC	peptide, a nucleotide sequence the NS-specific antigen or its analogue or	
CC	combinations. The method is useful for promoting nerve regeneration and	
CC	preventing neuronal degeneration in central/peripheral nervous system	
CC	from injury/disease, where the injury is spinal cord injury, blunt	
CC	trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or	
CC	autoimmune disease or neoplasm. The disease results in a degenerative	
CC	process occurring in either gray or white matter or both. The disease is	
CC	diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's	
CC	disease, facial nerve (Bell's) palsy, glioma, Huntington's chorea,	
CC	amyotrophic lateral sclerosis, non-artritic optic neuropathy, and	
CC	vitamin deficiency, intervertebral disc herniation, prion diseases such	
CC	as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral	
CC	neuropathies associated with various diseases, including but not limited	
CC	to uremia, porphyria, hypoglycemia, Sjogren Larsson syndrome, acute	
CC	sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary	
CC	amyloidosis, obstructive lung diseases, acromegaly, malabsorption	
CC	syndromes, polycythemia vera, immunoglobulin (Ig)- and IgG gamma-	
CC	pathies, complications of various drugs (e.g. metronidazole) and toxins	
CC	(e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia	
CC	relating to Friedreich's ataxia, amyloid polynuropathies, and Fabry's	
CC	adrenomyeloneuropathy, Giant axonal neuropathy, Reissner's disease, Fabry's	
CC	disease, or lipoproteinemia. The present sequence represents the rat	
CC	neurotransmitter receptor protein Nogo-A, an example of NS-specific	
CC	antigen	
XX		
XX	Sequence 1163 AA;	
XX		
XX	Query Match 100.0%; Score 139; DB 5; Length 1163;	
XX	Best Local Similarity 100.0%; Pred. No. 9.7e-07;	
XX	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

```

QY      1  EPDEDEDEDEDEDEDEDEDELELEVL 27
      31  EPDEDEDEDEDEDEDEDEDELELEVL 57

Db

RESULT 12
ADP45572
ID  ADP45572 standard; protein; 1163 AA.
AC  ADP45572;
XX
XX  ADP45572;
XX
DT  29-JUL-2004 (first entry)
DE  Rat truncated Nogo-A protein.
XX
XX  rat; human; Nogo-A; truncated; affinity; membrane-bound protein.
XX
XX  Rattus sp.
XX
XX  WO2004039836-A1.
XX
XX  13-MAY-2004.
XX
XX  31-OCT-2002; 2002WO-BP012210.
XX
XX  31-OCT-2002; 2002WO-BP012210.
XX
XX  (PIER-) PIERIS PROTEOLAB AG.
XX
XX  Skerra A, Fiedler M;
XX
XX  WPI; 2004-376159/35.
XX
XX  New isolated truncated Nogo-A polypeptide that corresponds to a truncated
XX  form of the Nogo-A protein, useful for identifying a compound having
XX  detectable affinity to a Nogo-A protein.
XX
XX  Claim 1; Fig 6A; 80pp; English.
XX
XX  The present invention relates to an isolated truncated Nogo-A polypeptide
XX  that corresponds to a truncated form of the Nogo-A protein from the rat
XX  and from the human. The truncated polypeptide is useful for identifying a
XX  compound having detectable affinity to a Nogo-A protein. The present
XX  sequence is a Nogo-A polypeptide of the invention.
XX
XX  Sequence 1163 AA;
XX
XX  Query Match 100.0%; Score 139; DB 8; Length 1163;
XX  Best Local Similarity 100.0%; Pred. No. 9,78-07;
XX  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1  EPDEDEDEDEDEDEDEDEDELELEVL 27
      31  EPDEDEDEDEDEDEDEDEDELELEVL 57

Db

RESULT 13
ADP45572
ID  ADP45572 standard; protein; 1163 AA.
AC  ADP45572;
XX
XX  ADP45572;
XX
DT  09-SEP-2004 (first entry)
DE  Rat NogoA protein SEQ ID NO:26.
XX
XX  binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
XX  nerve repair; neuroprotective; gene therapy;
XX  central nervous system injury; CNS injury; neurodegenerative disorder;
XX  rat.
XX
XX  Rattus norvegicus.
XX

```

XX PN W02004052932-A2.
XX DD 24-JUN-2004.
XX PF 09-DEC-2003; 2003WO-EP013960.
XX PR 10-DEC-2002; 2002GB-00028832.
XX PA (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS PHARMA GMBH.
XX PA (UYZU-) UNIV ZUERICH.
XX PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
XX PI Zurini M;
XX DR WPI; 2004-468818/44.
XX DR N-PSDB; ADP45571.
XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
XX Example 1; SEQ ID NO 26; 121pp; English.
XX The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 100nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents rat NogoA, which is used in the exemplification of the present invention.
XX Sequence 1163 AA;
XX
XX Query March 100.0%; Score 139; DB 8; Length 1163;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-07;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
XX DB 31 EPDEDEDEDEDEDEDEDEDEDELEVL 57
XX
XX RESULT 14
XX ADZ07609
XX ID ADZ07609 standard; protein; 1163 AA.
XX AC ADZ07609;
XX
XX 16-JUN-2005 (first entry)
XX Rat NogoA polypeptide.
XX antibody; NogoA; pharmaceutical; peripheral neuropathy;
XX central nervous system disease; neurodegenerative disease;
XX Alzheimers disease; Parkinsons disease; motor neurone disease;
XX ocular disease; diabetic retinopathy; age related macular degeneration;
XX myopia; cns-gen; neuroprotective; nootropic; antiparkinsonian;
XX antidiabetic; ophthalmological.
XX
XX Rattus norvegicus.
XX
XX WO2005028508-A2.
XX
XX 31-MAR-2005.
XX
XX 17-SEP-2004; 2004WO-EP010489.

XX 19-SEP-2003; 2003GB-00021997.
XX (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS PHARMA GMBH.
XX PA (UYZU-) UNIV ZURICH.
XX PI Barske C, Frentzel S, Mir AK, Schwab ME, Vitaliti A;
XX DR WPI; 2005-242564/25.
XX DR N-PSDB; ADZ07608.
XX New binding molecule capable of binding to human NogoA polypeptide, human NiG, human NiG-D20, or human NogoA342-357, useful for treating nerve repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral sclerosis.
XX Disclosure; SEQ ID NO 26; 117pp; English.
XX The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable of binding to human NogoA polypeptide (SEQ ID NO: 5), human NiG polypeptide (SEQ ID NO: 7), human NiG-D20 polypeptide (SEQ ID NO: 24), or human NogoA 342-357 (SEQ ID NO: 6) all given in the specification, with a dissociation constant of less than 100nM. The binding molecule of the invention comprises a first antigen binding site comprising in sequence the hypervariable regions CDR-H1, CDR-H2, and CDR-H3, where each of the hypervariable regions are at least 50% homologous to their equivalent hypervariable regions CDR-H1-3A6 (SEQ ID NO: 8), CDR-H2-3A6 (SEQ ID NO: 9), and CDR-H3-3A6 (SEQ ID NO: 10) all given in the specification, and a second antigen binding site comprising in sequence the hypervariable regions CDR-L1, CDR-L2, and CDR-L3, where each of the hypervariable regions are at least 50% homologous to their equivalent hypervariable regions CDR-L1-3A6 (SEQ ID NO: 11), CDR-L2-3A6 (SEQ ID NO: 12), and CDR-L3-3A6 (SEQ ID NO: 13) all given in the specification. Also described are: (i) polynucleotide sequences encoding the binding molecules above, (ii) polynucleotide sequences comprising fully defined sequences (SEQ ID Nos 14-19) given in the specification, (iii) an expression vector comprising the polynucleotide sequences above, where the expression system or its part is capable of producing a polypeptide, when the expression system or its part is present in a compatible host cell, (iv) an isolated host cell comprising the expression system above, (v) a pharmaceutical composition comprising the binding molecule in association with at least one pharmaceutical carrier or diluent, and (vi) a method of treating diseases associated with nerve repair. The binding molecules of the invention are useful as a pharmaceutical, preferably in the treatment of nerve repair. They are also useful in the treatment of various diseases of the peripheral (PNS) and central (CNS) nervous system, e.g. neurodegenerative diseases including Alzheimer's disease, Parkinson's disease, or amyotrophic lateral sclerosis. The binding molecules may also be used for treating degenerative ocular disorders including diabetic retinopathy, age-related macular degeneration, or pathologic myopia. This sequence represents rat NogoA polypeptide. Note: This sequence given as SEQ ID No.26 in the sequence listing is not mentioned elsewhere in the specification.
XX Sequence 1163 AA;
XX
XX Query Match 100.0%; Score 139; DB 9; Length 1163;
XX Best Local Similarity 100.0%; Pred. No. 9.7e-07;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
XX DB 31 EPDEDEDEDEDEDEDEDEDEDELEVL 57
XX
XX RESULT 15
XX ADT89537
XX ID ADT89537 standard; protein; 1162 AA.
XX AC ADT89537;
XX
XX 16-DEC-2004 (first entry)

XX Mus musculus Nogo protein.
DE
XX Nerve regeneration; gene therapy; vaccine; neuroprotective; nootropic;
KW Nogo; mouse.
XX
XX Mus musculus.
OS
XX US2004191240-A1.
PN
XX 30-SEP-2004.
PD
XX 31-JUL-2003; 2003US-00633423.
PF
XX 28-MAR-2003; 2003JP-00092923.
PR
XX 30-APR-2003; 2003US-00427741.
PP
XX (TOHY/) TOHYAMA M.
PA (YANA/) YAMASHITA T.
XX
XX Tohyama M, Yamashita T;
PI
XX WPI, 2004-698659/68.
DR N-PSDB; ADI89536.
DR
XX Regenerating nerves or modulating nerve regeneration comprises inhibiting
PT or modulating p75 signal transduction pathway by administering a
PT transduction agent, e.g. p21 or Rho, or an agent that interacts with the
PT transduction agent.
PT
XX
XX Example 2; SEQ ID NO 10; 209pp; English.
PS
XX The present invention relates to a method for regenerating nerves or
XX modulating nerve regeneration. The method involves inhibiting or
CC modulating a p75 signal transduction pathway. The invention is useful for
CC treating, preventing or diagnosing neurological diseases based on nerve
CC regeneration and for identifying agents useful for nerve regeneration.
CC The invention is also useful in gene therapy and for preparing vaccine.
CC The present sequence is the Mus musculus Nogo protein. Note: This
CC sequence is said to be encoded by SEQ ID NO 9, however this does not appear
CC to be the same.
XX
XX Sequence 1162 AA;
SQ
Query Match 86.0%; Score 119.5; DB 8; Length 1162;
Best Local Similarity 92.6%; Pred. No. 0.00012;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 EFDEDEDEDEDEDEDEDELEVL 27
DB 31 EFDEDEDEDEE-EEDEDEDELEVL 56
Search completed: February 17, 2006, 03:49:29
Job time : 127.333 secs

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A:Gene: CESP:RIIA5.1a
A:Map position: 1
A:Introns: 14/2; 40/3; 277/3; 318/3; 363/3; 560/1; 668/1; 808/3
Query Match 66.9%; Score 93; DB 2; Length 906;
Best Local Similarity 68.0%; Pred. No. 0.22;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EPDEDEDEDEDEDEDEDEDELE 25
Db 586 EDDDEDEDEDEDEDEDEDEDE 610
RESULT 8
T10455
heat shock related protein - Plasmodium berghei
C:Species: Plasmodium berghei
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10455
R:Wiser, M.F.; Jennings, G.J.; Uparankuraw, P.; van Belkum, A.; Doorn, L.J.; Kumar, N.
Mol. Biochem. Parasitol. 83, 25-33, 1996
A:Title: Further characterization of a 58 kDa Plasmodium berghei phosphoprotein as a co-
A:Reference number: Z17026; MUID:97164116; PMID:9010839
A:Accession: T10455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-376 <WIS>
A:Cross-references: UNIPROT:Q08168; UNIPARC:UPI000016BF72; EMBL:L04508; NID:g309691; PID
A:Experimental source: strain ANKA
C:Keywords: molecular chaperone
Query Match 66.2%; Score 92; DB 2; Length 376;
Best Local Similarity 59.3%; Pred. No. 0.12;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EPDEDEDEDEDEDEDEDEDELE 27
Db 14 EKSDDEDEDEDEDEDDPEKLELI 40
RESULT 9
A34719
nonhistone chromosomal protein HMG-2 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34719
R:Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A:Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle
A:Reference number: A34719; MUID:90275208; PMID:2350545
A:Accession: A34719
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-210 <SHI>
A:Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN
C:Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C:Keywords: chromosomal protein; DNA binding; nucleus
P:6-83/Domain; HMG box homology <HMG1>
F:92-166/Domain; HMG box homology <HMG2>
Query Match 65.1%; Score 90.5; DB 2; Length 210;
Best Local Similarity 76.0%; Pred. No. 0.093;
Matches 19; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
Qy 1 EPDEDEDEDEDEDEDEDEDELE 22
Db 186 EPDEDEDEDEDEDEDEDEDEDE 210
RESULT 10
S02708
tropoinin T - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Feb-1997
C:Accession: S02708
R:Sullard, B.; Leonard, K.; Larkins, A.; Butcher, G.; Karlík, C.; Fyrberg, E.
J. Mol. Biol. 204, 621-637, 1988
A:Title: tropoinin of asynchronous flight muscle.
A:Reference number: S02708; MUID:89141761; PMID:2852258
A:Accession: S02708
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-387 <BLU>
A:Cross-references: UNIPARC:UPI000017BEE2
C:Genetics:
A:Gene: FlyBase:up
A:Cross-references: FlyBase:FBgn0004169
C:Keywords: muscle
Query Match 64.7%; Score 90; DB 2; Length 387;
Best Local Similarity 68.0%; Pred. No. 0.18;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EPDEDEDEDEDEDEDEDELE 25
Db 348 EEDDEDEDEDEDEDEDEDEEE 372
RESULT 11
S13251
tropoinin T - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S13251; S29482
R:Fyrberg, E.; Fyrberg, C.C.; Beall, C.; Saville, D.L.
J. Mol. Biol. 210, 657-675, 1990
A:Title: Drosophila melanogaster tropoinin-T mutations engender three distinct syndromes
A:Reference number: S13251; MUID:91080155; PMID:2124273
A:Accession: S13251
A:Molecule type: mRNA
A:Residues: 1-396 <FYRI>
A:Cross-references: UNIPROT:P19351; UNIPARC:UPI000017BEE3; EMBL:X54504
R:Fyrberg, E.A.
submitted to the EMBL Data Library, August 1990
A:Reference number: S29482
A:Accession: S29482
A:Molecule type: mRNA
A:Residues: 1-191, 'A', 193-396 <FYR2>
A:Cross-references: UNIPARC:UPI0000137662; EMBL:X54504; NID:g8739; PID:g8740
C:Genetics:
A:Gene: FlyBase:up
A:Cross-references: FlyBase:FBgn0004169
A:Map position: X
Query Match 64.7%; Score 90; DB 2; Length 396;
Best Local Similarity 68.0%; Pred. No. 0.19;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EPDEDEDEDEDEDEDEDELE 25
Db 357 EEDDEDEDEDEDEDEDEDEEE 381
RESULT 12
B35041
ryanodine receptor, skeletal muscle - rabbit
N:Alternate names: calcium-release channel protein; junctional channel complex
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 27-Jul-1990 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C:Accession: S04654; B35041; A36181; S53794; S32504
R:Takehashima, H.; Nishimura, S.; Matsumoto, I.; Ishida, H.; Kangawa, K.; Minamino, N.; Mat
Nature 339, 439-445, 1989
A:Title: Primary structure and expression from complementary DNA of skeletal muscle ryan
A:Reference number: S04654; MUID:89262082; PMID:2725677
A:Accession: S04654
A:Molecule type: mRNA

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 03:43:13 ; Search time 123.333 Seconds
(without alignments)
154.453 Million cell updates/sec

Title: US-09-830-972A-2_COPY_31_57

Perfect score: 139

Sequence: 1 BPDEDEDEDEDEDEDEDELEVL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	139	100.0	360	Q6IRL3 RAT	Q6ir13 rattus norv
2	139	100.0	379	Q540J3 RAT	Q540j3 rattus norv
3	139	100.0	478	Q5UI23 RAT	Q5ul23 rattus norv
4	139	100.0	1163	1 RTN4 RAT	Q9jk11 rattus norv
5	119.5	86.0	356	2 Q8BH78 MOUSE	Q8bh78 mus musculu
6	119.5	86.0	375	2 Q8K3G7 MOUSE	Q8k3g7 mus musculu
7	119.5	86.0	375	2 Q8BH75 MOUSE	Q8bh75 mus musculu
8	119.5	86.0	720	2 Q7TNB7 MOUSE	Q7tnb7 mus musculu
9	119.5	86.0	1162	2 Q8BGM9 MOUSE	Q8bgm9 mus musculu
10	119.5	86.0	1163	2 Q8K3G8 MOUSE	Q8k3g8 mus musculu
11	119.5	86.0	1245	2 Q5DTR9 MOUSE	Q5dtr9 mus musculu
12	111.5	80.2	185	2 Q53R94 HUMAN	Q53r94 homo sapien
13	111.5	80.2	373	2 Q7L7Q6 HUMAN	Q7l7q6 homo sapien
14	111.5	80.2	392	2 Q96B16 HUMAN	Q96b16 homo sapien
15	111.5	80.2	1192	1 RTN4 HUMAN	Q9nqc3 homo sapien
16	111.5	80.2	1192	2 Q7L7Q8 HUMAN	Q7l7q8 homo sapien
17	100	71.9	343	2 Q61PN0 HUMAN	Q61pn0 homo sapien
18	99.5	71.6	306	2 Q6Z867 ORYZA	Q6z867 oryza sativ
19	97	69.8	208	1 HMG2 HUMAN	Q26583 homo sapien
20	97	69.8	209	2 Q5U072 HUMAN	Q5u072 homo sapien
21	97	69.8	496	2 Q6Q138 RAT	Q6q138 rattus norv
22	97	69.8	792	2 Q9YTL7 9HERP	Q9ytl7 ateline her
23	96	69.1	222	2 Q6PUE4 BRABE	Q6pue4 brachyosteo
24	96	69.1	456	2 Q5GF04 BRARE	Q5gf04 brachyosteo
25	96	69.1	496	2 Q5RIZ4 BRARE	Q5riz4 brachyosteo
26	96	69.1	639	2 Q8LIY6 PLAF7	Q8liy6 plasmodium
27	96	69.1	2649	2 Q7RAS7 PLAYO	Q7ras7 plasmodium
28	95	68.3	209	1 HMG2 MOUSE	Q30681 mus musculu
29	95	68.3	746	2 Q54VB9 D1C1	Q54vb9 dictyosteli
30	95	68.3	1205	2 Q54J58 D1C1	Q54j58 dictyosteli
31	94	67.6	227	1 CHIC1_MOUSE	Q8cbw7 mus musculu

Q94K07 arabidopsis
Q9Ltc5 arabidopsis
Q9tx81 plasmodium
Q6l796 ipomoea pur
Q6inq5 xenopus lae
Q5c954 cryptospori
Q36421 alcelaphine
Q4yu61 plasmodium
Q54kk9 dictyosteli
Q7m732 mus musculu
Q90228 ambystoma m
Q5l317 entamoeba h
Q4scs8 tetraodon n
Q4xmw2 plasmodium

32 94 67.6 374 2 Q94K07 ARATH
33 94 67.6 374 2 Q9LTS5 ARATH
34 94 67.6 407 2 Q9TX81 PLACH
35 94 67.6 665 2 Q6L796 IPOPU
36 94 67.6 683 2 Q6INQ5 XENLA
37 94 67.6 1274 2 Q5CQ54 CRYPV
38 94 67.6 1300 2 Q36421 9GAMA
39 94 67.6 1428 2 Q4YU61 PLABE
40 94 67.6 1472 2 Q54KK9 D1C1
41 94 67.6 1746 2 Q7M732 MOUSE
42 93 66.9 216 2 Q90228 AMBME
43 93 66.9 235 2 Q5L317 ENTHI
44 93 66.9 300 2 Q4SCS8 TETNG
45 93 66.9 391 2 Q4XMW2 PLACH

ALIGNMENTS

RESULT 1

Q6IRL3 RAT PRELIMINARY; PRT; 360 AA.
AC Q6IRL3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Rtn4 protein (RTN4-B1).
GN Name=Rtn4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung and Placenta;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung R.;
RX Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22715987; PubMed=12832288;
RA Certle T., Klingner M., Stuermer C.A., Schwab M.E.;
RT "A reticular rapapody: phylogenetic evolution and nomenclature of the
RT RTN/Nogo gene family".
RN FASEB J. 17:1238-1247(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;

Tue Feb 21 15:13:29 2006

Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RA EMBL; BC070879; AAH70879.1; -; mRNA.
 RA EMBL; AY164740; AAH74740.1; -; mRNA.
 RA EMBL; BC097936; AAH97936.1; -; mRNA.
 RA GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; P50845; RETICULON; 1.
 SQ SEQUENCE 360 AA; 38822 MW; 149714AD6C3D65A7 CRC64;

Query Match 100.0%; Score 139; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
 |||||
 DB 31 EPDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 2
 ID Q5UI23 RAT PRELIMINARY; PRT; 379 AA.

AC 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE RTN4-B2;
 GN Name=Rtn4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Oertle T., Klingner M., Stuermer C.A., Schwab M.E.;
 "A reticular rhabdomy; Phylogenetic evolution and nomenclature of the
 RT RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164741; AAP47316.1; -; mRNA.
 SQ SEQUENCE 379 AA; 40719 MW; 9F15AB942D36ED0F CRC64;

Query Match 100.0%; Score 139; DB 2; Length 379;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
 |||||
 DB 31 EPDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 3
 ID Q5UI23 RAT PRELIMINARY; PRT; 478 AA.

AC Q5UI23;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Rtn4 protein (Fragment).
 GN Name=Rtn4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Tissue=Heart;
 RC STRAIN=Sprague-Dawley; Tissue=Adipocyte;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krywinski M.I., Skalska U., Smalish U.,
 RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC Tissue=Heart;
 RG NIH MOC Project;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC086375; AAH6375.1; -; mRNA.

FT NON_TER 478 478
 SQ SEQUENCE 478 AA; 51326 MW; B5A1E421A3541D2A CRC64;

Query Match 100.0%; Score 139; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDEDEDEDEDEDEDEDEDELELEVL 27
 |||||
 DB 31 EPDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 4

RTN4 RAT STANDARD; PRT; 1163 AA.
 AC Q9JX11; Q9JX10; Q9R009; Q9WU09; Q9WU00;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)
 DE (Glut4 vesicle 20 kDa protein).
 GN Name=Rtn4; Synonym=Nogo;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 3), AND PARTIAL PROTEIN SEQUENCE.

RA STRAIN=Sprague-Dawley; Tissue=Adipocyte;
 RC MEDLINE=99249816; PubMed=10231557; DOI=10.1016/S0167-4889(99)00033-6;
 RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
 "Cloning and characterization of a 22 kDa protein from rat adipocytes:
 FT a new member of the reticulon family.";
 RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
 EN MEDLINE=20129258; PubMed=10667796; DOI=10.1038/35000219;
 EX Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A., Christ F., Schwab M.E.;
 "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1.";
 RL Nature 403:434-439(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 4).
 RC STRAIN=Wistar Kyoto; Tissue=Vascular smooth muscle;
 RA Ito T., Schwartz S.M.;
 RT Cloning of a member of the reticulon gene family in rat: one of two
 minor splice variants";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.


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Db          31 EPEDEDEDEE-EEDEDELELEVL 56

RESULT 6
Q8K3G7_MOUSE
ID Q8K3G7_MOUSE PRELIMINARY; PRT; 357 AA.
AC Q8K3G7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nogo-B.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Jin W., Li R., Long M., Shen J., Ju G.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY114153; AAM77069.1; -; mRNA.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0042995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005783; C:protein binding; IPI.
DR GO; GO:0005152; P:angiogenesis; IMP.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFBDF15 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 357;
Best Local Similarity 92.6%; Pred. NO. 0.0082;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEE-EEDEDELELEVL 27
DB 31 EPEDEDEDEE-EEDEDELELEVL 56

RESULT 7
Q8BHFS_MOUSE
ID Q8BHFS_MOUSE PRELIMINARY; PRT; 375 AA.
AC Q8BHFS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE RTN4 (Reticulon 4).
GN Name=rtn4; ORFNames=RP23-17605.4-006;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7; and 129/SvcJ7;
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
RT human and mouse nogo/rtn4."
RL J. Mol. Biol. 325:299-323(2003).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvcJ7;
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6; TISSUE=Brain;

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RC STRAIN=129SVCJ7;
RA Van der Putten H., Mir A.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RP Kay M.;
RA Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY102282; AAM73504.1; -; mRNA.
DR EMBL; AY102286; AAM73509.1; -; Genomic DNA.
DR EMBL; AL929371; CA12421.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000020458; Mus musculus.
DR MGI; MGI:1915835; Rtn4.
DR GO; GO:0042995; C:cell projection; IDA.
DR GO; GO:0043025; C:cell soma; IDA.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0005152; P:angiogenesis; IMP.
DR GO; GO:0001525; P:angiogenesis; IMP.
DR GO; GO:0007399; P:neurogenesis; IDA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 375;
Best Local Similarity 92.6%; Pred. NO. 0.0086;
Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPEDEDEDEE-EEDEDELELEVL 27
DB 31 EPEDEDEDEE-EEDEDELELEVL 56

RESULT 8
Q7TNB7_MOUSE
ID Q7TNB7_MOUSE PRELIMINARY; PRT; 720 AA.
AC Q7TNB7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Name=Rtn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Balwstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bana S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madao A., Rodrigues S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;

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RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC056373; AAH56373.1; -, mRNA.
 DR MGI; MGI:1915835; Rtn4.
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005151; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 KW Hypothetical protein.
 SQ SEQUENCE 720 AA; 77435 MW; 80AB78728F16EAB2 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 720;
 Best Local Similarity 92.6%; Pred. No. 0.016;
 Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
 |||||:|||||
 Db 31 EPDEDEDEDEDEDEDEDEDELEVL 56

RESULT 9

ID Q8BG9_MOUSE PRELIMINARY; PRT; 1162 AA.
 AC Q8BG9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Rtn4 (Reticulon 4).
 GN Name=Rtn4; ORFNames=RP23-17605.4-005;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SVCJ7, and 129SVcJ7;
 RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
 RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
 RT "Genomic structure and functional characterisation of the promoters of
 human and mouse nogo/rtn4.";
 RJ J. Mol. Biol. 325:299-323(2003).
 RW [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SVCJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129SVcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Kay M.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY102284; AAM73506.1; -, mRNA.
 DR EMBL; AY102286; AAM73511.1; -, Genomic DNA.
 DR EMBL; AL929371; CA124273.1; -, Genomic DNA.
 DR Ensembl; ENSMUSG0000020458; Mus musculus.
 DR MGI; MGI:1915835; Rtn4.
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005151; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 DR SEQUENCE 1162 AA; 126612 MW; 855697FBEE11781F CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 1162;
 Best Local Similarity 92.6%; Pred. No. 0.024;
 Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
 |||||:|||||
 Db 31 EPDEDEDEDEDEDEDEDEDELEVL 56

RESULT 10

ID Q8K3G_MOUSE PRELIMINARY; PRT; 1163 AA.
 AC Q8K3G;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nogo-A.
 GN Name=Rtn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Jin W., Long M., Li R., Ju G.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY114152; NAM77068.1; -, mRNA.
 DR MGI; MGI:1915835; Rtn4
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005151; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 DR SEQUENCE 1163 AA; 126690 MW; 6B5F362799417EA4 CRC64;

Query Match 86.0%; Score 119.5; DB 2; Length 1163;
 Best Local Similarity 92.6%; Pred. No. 0.024;
 Matches 25; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
 |||||:|||||
 Db 31 EPDEDEDEDEDEDEDEDEDELEVL 56

RESULT 11

ID Q5DTK9_MOUSE PRELIMINARY; PRT; 1245 AA.
 AC Q5DTK9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE KIAA4153 protein (Fragment).
 GN Name=Rtn4; Synonym=KIAA4153;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fetal brain;
 RA Okazaki N., Kikuno R.P., Ohara R., Inamoto S., Nagase T., Ohara O.,
 RA Koga H.;
 RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene.
 The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs
 Identified by Screening of Terminal sequences of cDNA Clones Randomly

RT Sampled from Size-Fractionated Libraries. ";
 RL EMBL; AK220511; BAD90301.1; -; mRNA.
 DR MGI; MGI:1915835; Rtn4.
 DR GO; GO:0042995; C:cell projection; IDA.
 DR GO; GO:0043025; C:cell soma; IDA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0001525; P:angiogenesis; IMP.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00845; RETICULON; 1.
 FT NON TER 1
 SQ SEQUENCE 1245 AA; 135257 MW; 85460D746CE7F16C CRC64;
 Query Match 86.0%; Score 119.5; DB 2; Length 1245;
 Best Local Similarity 92.6%; Pred. No. 0.026; Mismatches 1; Indels 1; Gaps 1;
 Matches 25; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
 DB 114 EPEDEDEDEDEDEDEDEDEDEDELEVL 139
 RESULT 12
 OS Homo sapiens (Human).
 ID Q53R94 HUMAN PRELIMINARY; PRT; 185 AA.
 AC Q53R94;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein Rtn4 (Fragment).
 GN Name=Rtn4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kozlowicz A., Doebber A., Trani L.;
 RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC093165; AY24029.1; -; Genomic DNA.
 DR EMBL; AC093165; AY24029.1; -; Genomic DNA.
 KW Hypothetical protein.
 FT NON TER 185
 SQ SEQUENCE 185 AA; 19300 MW; 568DF2FF3EBBF3E8 CRC64;
 Query Match 80.2%; Score 111.5; DB 2; Length 185;
 Best Local Similarity 85.2%; Pred. No. 0.022; Mismatches 3; Indels 1; Gaps 1;
 Matches 23; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
 DB 30 EPEDEDEDEDEDEDEDEDEDEDELEVL 55
 RESULT 13
 OS Homo sapiens (Human).
 ID Q7L706 HUMAN PRELIMINARY; PRT; 373 AA.
 AC Q7L706;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE "The sequence of Homo sapiens BAC clone Rp11-1255P17. ";
 DE Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 GN Name=Rtn4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC093165; AY24029.1; -; Genomic DNA.
 DR EMBL; AC093165; AY24029.1; -; Genomic DNA.
 KW Hypothetical protein.
 FT NON TER 185
 SQ SEQUENCE 185 AA; 19300 MW; 568DF2FF3EBBF3E8 CRC64;
 Query Match 80.2%; Score 111.5; DB 2; Length 185;
 Best Local Similarity 85.2%; Pred. No. 0.022; Mismatches 3; Indels 1; Gaps 1;
 Matches 23; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
 DB 30 EPEDEDEDEDEDEDEDEDEDEDELEVL 55

AC Q7L706;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE "Genomic structure and functional characterisation of the promoters of
 human and mouse rtg4. ";
 GN Name=RTN4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Van der Putten H.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY102277; AM64241.1; -; mRNA.
 DR EMBL; AY102277; AM64241.1; -; Genomic DNA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 SQ SEQUENCE 373 AA; 40317 MW; 8A19379EF91A59B4 CRC64;
 Query Match 80.2%; Score 111.5; DB 2; Length 373;
 Best Local Similarity 85.2%; Pred. No. 0.041; Mismatches 23; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 Matches 23; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 EPEDEDEDEDEDEDEDEDEDEDELEVL 27
 DB 30 EPEDEDEDEDEDEDEDEDEDEDELEVL 55
 RESULT 14
 OS Homo sapiens (Human).
 ID Q96B16 HUMAN PRELIMINARY; PRT; 392 AA.
 AC Q96B16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Reticulon 4, isoform D (RTN4 isoform B2).
 GN Name=RTN4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tissue=Kidney;
 RA MDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Carninci P.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Jones S.J.M., Smallos D.E.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Marra M.A.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22376540; PubMed=12488097; DOI=10.1016/S0022-2836(02)01179-8;
RA Oertle T., Huber C., van der Putten H., Schwab M.E.;
RT "Genomic structure and functional characterisation of the promoters of
human and mouse nogo/rtn4.";
RL J. Mol. Biol. 325:299-323 (2003).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Van der Putten H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016165; AAH16165.1; -; mRNA.
DR EMBL; AY102278; AAM64247.1; -; mRNA.
DR EMBL; AY102285; AAM64242.1; -; Genomic DNA.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS0845; RETICULON; 1.
SQ SEQUENCE 392 AA, 42274 MW, D7B2AA5E839B58AD CRC64;

Query Match 80.2%; Score 111.5; DB 2; Length 392;
Best Local Similarity 85.2%; Pred. No. 0.043; 0; Indels 1; Gaps 1;
Matches 23; Conservative 3; Mismatches 0;

QY 1 EPDEDEDEDEDEDEDEDEDELEVL 27
DB 30 EPDEDEDEDEDEDEDEDEDELEVL 55

RESULT 15
RTN4_HUMAN
ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; Q9A962; Q9BXG5; Q9H212; Q9H313; Q9U042; Q9Y293; Q9Y2V7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
protein C homolog) (RTN-x) (Reticulon 5).
DE Name=RTN4; Synonyms=ASY, KIAA0886, NOGO; ORFNames=My043, SP1507;
DE Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780; DOI=10.1038/35000287;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=2110696; PubMed=11126360; DOI=10.1038/sj.onc.1203948;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14--2p13 by radiation hybrid mapping.";

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RL Cytogetet. Cell Genet. 88:101-102 (2000).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.W.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RL "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RX PubMed=15498874; DOI=10.1073/pnas.0404089101;
RA Qiu D., Gong Y., Qin W., Zhang P., Li J., Wei L., Zhou X., Li H.,
Wan X., Zhong F., He L., Yu J., Yao G., Jiang H., Qian L., Yu Y.,
Shu H., Chen X., Xu H., Guo M., Pan Z., Chen Y., Ge C., Yang S.,
Gu J.;
RT "Large-scale cDNA transfection screening for genes related to cancer
development and progression.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:15724-15729 (2004).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Miyase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 5:355-364 (1998).
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Eye, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
PAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez R.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [11]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC TISSUE=Umbilical cord blood;
RX MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;

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RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang Q.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RT Genome Res. 10:1546-1560(2000).
RN [12]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 482-1192 (ISOFORMS 1/4).
RC TISSUE=Petal brain;
RC MAO Y.M., Xie Y., Zheng Z.H.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL [13]
RN NUCLEOTIDE SEQUENCE OF 186-1192 (ISOFORM 1).
RC TISSUE=Testis;
RC Sha J.H., Zhou Z.M., Li J.M.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL [14]
RN TOPOLOGY.
RC TISSUE=Brain;
RC MEDLINE=20129259; PubMed=10667797; DOI=10.1038/35000226;
RX Fournier A.E., Grandpre T., Strittmatter S.M.;
RA "Identification of the Nogo inhibitor of axon regeneration as a
RT Reticulon Protein.";
RL Nature 403:439-444(2000).
RN [15]
RN FUNCTION.
RC TISSUE=Brain;
RC MEDLINE=21069055; PubMed=11201742; DOI=10.1038/35053072;
RX Fournier A.E., Grandpre T., Strittmatter S.M.;
RA "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT regeneration.";
RL Nature 409:341-346(2001).
RN [16]
RN REVIEW.
RC MEDLINE=21888956; PubMed=11891768; DOI=10.1002/jnr.10134;
RX Ng C.E.L., Tang B.L.;
RA "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT regeneration.";
RL J. Neurosci. Res. 67:559-565(2002).
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC block the regeneration of the nervous central system in adults.
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC This is likely consecutive to their change in subcellular
CC location, from the mitochondria to the endoplasmic reticulum,
CC after binding and sequestration.
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum. Anchored to the membrane of the endoplasmic reticulum
CC through 2 putative transmembrane domains.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-XL;
CC IsoId=Q9NQC3-1; Sequence=Displayed;
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-XS, Foccen-M;
CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foccen-S;
CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC Name=4;
CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC widely expressed excepted for the liver. Isoform 3 is expressed in
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC specific.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -!- CAUTION: Ref.11 sequence differs from that shown due to
CC framehifts in positions 1149 and 1156.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not

removed.
CC -----
CC EMBL; AJ251383; CAB99248.1; -; mRNA.
DR EMBL; AJ251384; CAB99249.1; -; mRNA.
DR EMBL; AJ251385; CAB99250.1; -; mRNA.
DR EMBL; AB040462; BAB18927.1; -; mRNA.
DR EMBL; AB040463; BAB18928.1; -; mRNA.
DR EMBL; AF148537; AAG12176.1; -; mRNA.
DR EMBL; AF148538; AAG12177.1; -; mRNA.
DR EMBL; AF087901; AAG12205.1; -; mRNA.
DR EMBL; AF132047; AAG12206.1; -; mRNA.
DR EMBL; AF132048; AAD31022.1; -; mRNA.
DR EMBL; AB015639; BAA83712.1; -; mRNA.
DR EMBL; AF077050; AAD27783.1; -; mRNA.
DR EMBL; AF177332; AAG17976.1; -; mRNA.
DR EMBL; AB020693; BAA74909.2; ALT INIT; mRNA.
DR EMBL; BC001035; BAA10335.1; -; mRNA.
Query Match 80.2%; Score 111.5; DB 1; Length 1192;
Best Local Similarity 85.2%; Pred. No. 0.12;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
QY 1 EPDEDEDEDEDEDEDEDEDEDELEVL 27
DB 30 EPSDEE-EEEEDEDEDEDELEVL 55
Search completed: February 17, 2006, 03:55:48
Job time : 125.333 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2006, 03:56:08 ; Search time 28.6667 Seconds
(without alignments)
77.869 Million cell updates/sec

Title: US-09-830-972A-2_COPY_31_57
Perfect score: 139
Sequence: 1 EPEDEDEDEDEDEDEDEDELEVL 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/aaa/5 COMB.pep:*

2: /cgn2_6/ptodata/1/aaa/6 COMB.pep:*

3: /cgn2_6/ptodata/1/aaa/H COMB.pep:*

4: /cgn2_6/ptodata/1/aaa/PCTUS COMB.pep:*

5: /cgn2_6/ptodata/1/aaa/RE COMB.pep:*

6: /cgn2_6/ptodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB ID	Description
1	111.5	80.2	US-09-513-999C-6304	Sequence 6304, Ap
2	97.8	80.2	US-09-538-092-1018	Sequence 1018, Ap
3	97.8	208	US-09-214-881A-2	Sequence 2, Appli
4	97.8	320	US-09-949-016-10728	Sequence 10728, A
5	97.8	532	US-08-339-152A-32	Sequence 32, Appl
6	93.6	2079	US-09-949-016-8301	Sequence 8301, Ap
7	92.6	448	US-08-248-796A-15347	Sequence 15347, A
8	92.6	305	US-08-574-959A-9	Sequence 9, Appli
9	92.6	905	US-03-357-014-9	Sequence 9, Appli
10	92.6	1135	US-08-574-959A-7	Sequence 7, Appli
11	92.6	1135	US-09-357-014-7	Sequence 7, Appli
12	91.6	209	US-09-214-881A-8	Sequence 8, Appli
13	91.6	213	US-09-214-881A-6	Sequence 6, Appli
14	90.5	209	US-09-214-881A-10	Sequence 10, Appl
15	90.5	199	US-09-248-796A-22092	Sequence 22092, A
16	90.6	240	US-08-114-555A-8	Sequence 8, Appli
17	90.6	64.7	US-08-559-397A-14	Sequence 14, Appl
18	90.6	5037	US-09-424-783-4	Sequence 4, Appli
19	88.6	412	US-08-741-134-2	Sequence 2, Appli
20	88.6	683	US-10-104-047-2973	Sequence 2973, Ap
21	87.6	206	US-09-214-881A-9	Sequence 9, Appli
22	87.6	62.6	US-09-538-092-883	Sequence 883, App
23	87.6	214	US-09-214-881A-1	Sequence 1, Appli
24	87.6	714	US-08-990-114-3	Sequence 3, Appli
25	87.6	714	US-09-241-333-3	Sequence 3, Appli
26	86.6	687	US-10-104-047-2651	Sequence 2651, Ap
27	86.6	706	US-09-538-092-957	Sequence 957, App

28	86	61.9	747	2	US-09-949-016-10040	Sequence 10040, A
29	86	61.9	1162	1	US-08-728-323A-2	Sequence 2, Appli
30	86	61.9	1162	2	US-09-298-568-2	Sequence 2, Appli
31	86	61.9	1162	2	US-09-410-399-2	Sequence 2, Appli
32	86	61.9	1162	2	US-09-894-273-2	Sequence 2, Appli
33	86	61.9	1540	2	US-09-949-016-11382	Sequence 11382, A
34	86	61.9	1540	2	US-09-949-016-11383	Sequence 11383, A
35	86	61.9	1719	1	US-08-459-568-4	Sequence 4, Appli
36	86	61.9	1719	1	US-08-399-411-4	Sequence 4, Appli
37	86	61.9	1719	2	US-08-516-859A-4	Sequence 4, Appli
38	86	61.9	1719	2	US-08-586-472-4	Sequence 4, Appli
39	86	61.9	1719	2	US-09-528-706-4	Sequence 4, Appli
40	86	61.9	1719	2	US-10-024-450-4	Sequence 4, Appli
41	85.5	61.5	214	2	US-09-214-881A-3	Sequence 3, Appli
42	85.5	61.5	214	2	US-09-214-881A-4	Sequence 4, Appli
43	85	61.2	214	2	US-09-214-881A-5	Sequence 5, Appli
44	85	61.2	240	1	US-08-114-555A-6	Sequence 6, Appli
45	85	61.2	240	2	US-08-559-397A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-09-513-999C-6304

; Sequence 6304, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59 US2 REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 6304

; LENGTH: 68

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-513-999C-6304

Query Match 80.2%; Score 111.5; DB 2; Length 68;

Best Local Similarity 85.2%; Pred. No. 2.7e-05;

Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 EPEDEDEDEDEDEDEDEDELEVL 27

Db 30 EPEDEE-EPEDEDEDEDEDELEVL 55

RESULT 2

US-09-538-092-1018

; Sequence 1018, Application US/09538092

; Patent No. 6753314

; GENERAL INFORMATION:

; APPLICANT: Glot, Loic

; APPLICANT: Mansfield, Traci A.

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092

; CURRENT FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178,965

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CuraPatSeqFormatter Version 0.9

; SEQ ID NO 1018

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; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

Query Match          69.8%; Score 97; DB 2; Length 208;
Best Local Similarity 73.9%; Pred. No. 0.0024;
Matches 17; Conservative

QY 1 EPEDEDEDEDEDEDEDELE 23
Db 185 EPEDEDEDEDEDEDEDEDEDEDE 207

RESULT 3
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078;
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuo
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hicoshi
; APPLICANT: Okakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-2

Query Match          69.8%; Score 97; DB 2; Length 208;
Best Local Similarity 73.9%; Pred. No. 0.0024;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELE 23
Db 185 EPEDEDEDEDEDEDEDEDEDEDE 207

RESULT 4
US-09-949-016-10728
; Sequence 10728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 10728

; LENGTH: 320
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10728

Query Match          69.8%; Score 97; DB 2; Length 320;
Best Local Similarity 73.9%; Pred. No. 0.0036;
Matches 17; Conservative 1; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELE 23
Db 297 EPEDEDEDEDEDEDEDEDEDEDE 319

RESULT 5
US-08-339-152A-32
; Sequence 32, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-32

Query Match          69.8%; Score 97; DB 1; Length 532;
Best Local Similarity 80.0%; Pred. No. 0.0058;
Matches 20; Conservative 1; Indels 2; Gaps 1;

QY 3 EDEDEDEDEDEDEDEDEDEDEDELE 25
Db 172 EDEDEDEDEDEDEDEDEDEDEDEDE 196

RESULT 6
US-09-949-016-8301
; Sequence 8301, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8301
 ; LENGTH: 2079
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-8301

Query Match 66.9%; Score 93; DB 2; Length 2079;
 Best Local Similarity 72.0%; Pred. No. 0.053;
 Matches 18; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EPEDEDEDEDEDEDEDEDELE 25
 DB 1077 EEEEEEEEEEEEEEEEEEE 1101

RESULT 7
 US-09-248-796A-15347
 ; Sequence 15347, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 15347
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; US-09-248-796A-15347

Query Match 66.2%; Score 92; DB 2; Length 448;
 Best Local Similarity 77.3%; Pred. No. 0.016;
 Matches 17; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 3 EDEDEDEDEDEDEDEDELE 24
 DB 410 DEEEDEDEDEDEDEDEEE 431

RESULT 8
 US-08-574-959A-9
 ; Sequence 9, Application US/08574959A
 ; Patent No. 5962224
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaekyoon Shin, Inail Joong, Ratna K. Vadlamudi
 ; APPLICANT: and Jack L. Strominger
 ; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/574,959A
 ; APPLICATION NUMBER: US/08/574,959A
 ; FILING DATE: 19-DEC-95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: DFN-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 905 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-574-959A-9

Query Match 66.2%; Score 92; DB 1; Length 905;
 Best Local Similarity 68.0%; Pred. No. 0.031;
 Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EPEDEDEDEDEDEDEDEDELE 25
 DB 665 EEEEEEEEEEEEEEEEEEE 689

RESULT 9
 US-09-357-014-9
 ; Sequence 9, Application US/09357014
 ; Patent No. 6291645
 ; GENERAL INFORMATION:
 ; APPLICANT: Jaekyoon Shin, Inail Joong, Ratna K. Vadlamudi
 ; APPLICANT: and Jack L. Strominger
 ; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/357,014
 ; FILING DATE: 19-Jul-1999
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/574,959
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: DFN-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 905 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

us-09-830-972a-2_copy_31_57.ra1

Tue Feb 21 15:13:29 2006

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; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-357-014-9
Query Match 66.2%; Score 92; DB 2; Length 905;
Best Local Similarity 68.0%; Pred. No. 0.031;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDELE 25
Db 665 EEEEEEEEEEEEEDEDEDEDE 689

RESULT 10
US-08-574-959A-7
; Sequence 7, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-959A-7
Query Match 66.2%; Score 92; DB 1; Length 1135;
Best Local Similarity 68.0%; Pred. No. 0.038;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDELE 25
Db 895 EEEEEEEEEEEEEDEDEDEDE 919

RESULT 11
US-09-357-014-7
; Sequence 7, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD

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; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/357,014
; FILING DATE: 19-Jul-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/574,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-357-014-7
Query Match 66.2%; Score 92; DB 2; Length 1135;
Best Local Similarity 68.0%; Pred. No. 0.038;
Matches 17; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDELE 25
Db 895 EEEEEEEEEEEEEDEDEDEDE 919

RESULT 12
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-8
Query Match 65.5%; Score 91; DB 2; Length 209;
Best Local Similarity 64.0%; Pred. No. 0.01;
Matches 16; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDEDELE 25

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Db      185 EPEDEDEDEDEDEDEDEDE 209

RESULT 13
US-09-949-016-10813
; Sequence 10813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 10813
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10813

Query Match      65.5%; Score 91; DB 2; Length 213;
Best Local Similarity 68.0%; Pred. No. 0.01;
Matches 17; Conservative 5; Mismatches 0; Indels 3; Gaps 0;

QY      1 EPEDEDEDEDEDEDEDEDELE 25
Db      189 EPEDEDEDEDEDEDEDEDE 213

RESULT 14
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuo
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-6

Query Match      65.1%; Score 90.5; DB 2; Length 209;
Best Local Similarity 76.0%; Pred. No. 0.012;
Matches 19; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY      1 EPEDEDEDEDEDEDEDEDELE 22
Db      185 EPEDEDEDEDEDEDEDEDE 209

RESULT 15

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US-09-248-796A-22092
; Sequence 22092, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22092
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22092

Query Match      64.7%; Score 90; DB 2; Length 199;
Best Local Similarity 73.9%; Pred. No. 0.012;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPEDEDEDEDEDEDEDELE 23
Db      89 EDEDEDEDEDEDEDEDEEE 111

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OM protein - protein search, using sw model

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Sequence: 1 EPEDEDEDEDEDEDEDELEVL 27

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- 5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	100.0	1163	7	US-11-044-899-2
2	139	100.0	1163	7	US-11-044-899-30
3	111.5	80.2	414	6	US-10-821-234-1170
4	111.5	80.2	1178	7	US-11-044-899-29
5	88	63.3	683	7	US-11-072-512-2973
6	88	63.3	773	7	US-11-169-041-213
7	87	62.6	215	6	US-10-821-234-143
8	86	61.9	482	6	US-10-821-234-1413
9	86	61.9	687	7	US-11-072-512-2651
10	84	60.4	144	6	US-10-821-234-1254
11	83	59.7	251	6	US-10-528-031-8
12	83	59.7	345	7	US-11-024-959-415
13	82	59.0	1299	7	US-11-054-281-107
14	81	58.3	417	6	US-10-821-234-1536
15	81	58.3	740	7	US-11-124-367A-293
16	81	58.3	760	7	US-11-124-367A-292
17	81	58.3	823	7	US-11-166-892-4
18	79	56.8	268	7	US-11-072-512-3158
19	79	56.8	879	7	US-11-169-041-192
20	78	56.1	3375	7	US-11-044-111-23
21	77.5	55.8	587	6	US-10-453-372-964
22	77.5	55.8	591	6	US-10-453-372-952
23	77.5	55.8	591	6	US-10-453-372-956
24	77.5	55.8	596	6	US-10-453-372-954
25	77.5	55.8	642	6	US-10-453-372-962

26	77.5	55.8	646	6	US-10-453-372-958
27	77.5	55.8	646	6	US-10-453-372-960
28	77.5	55.8	687	7	US-11-156-163-4
29	77.5	55.8	688	6	US-10-453-372-950
30	77.5	55.8	688	6	US-10-453-372-968
31	77.5	55.8	688	6	US-10-453-372-970
32	77	55.4	427	6	US-10-718-807-122
33	77	55.4	699	7	US-11-138-682-4
34	77	55.4	699	7	US-11-138-852-3
35	77	55.4	4374	7	US-11-128-572-2
36	76.5	55.0	645	6	US-10-821-234-1409
37	76	54.7	432	7	US-11-055-822-1096
38	75	54.0	298	6	US-10-821-234-1167
39	75	54.0	476	7	US-11-124-368A-261
40	75	54.0	619	7	US-11-124-368A-260
41	75	54.0	655	7	US-11-124-368A-262
42	75	54.0	671	7	US-11-124-368A-259
43	75	54.0	763	6	US-10-821-234-1619
44	75	54.0	1017	7	US-11-054-281-108
45	75	54.0	1061	7	US-11-121-438-4

ALIGNMENTS

RESULT 1
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED THEREON
; FILE OF INVENTION: 0200-017-999
; FILE REFERENCE: 0200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
US-11-044-899-2

Query Match 100.0%; Score 139; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEDEDEDEDEDEDEDELEVL 27
Db 31 EPEDEDEDEDEDEDELEVL 57

RESULT 2
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED THEREON
; FILE OF INVENTION: 10200-017-999
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972

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; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; SOFTWARE: FastSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 30
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus sp.
; NAME/KEY: VARIANT
; LOCATION: (1)...((1163) at all Xaa position
; OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30

Query Match      100.0%; Score 139; DB 7; Length 1163;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPEDEDEDEDEDEDEDEDEDEDELELEVL 27
Db 31 EPEDEDEDEDEDEDEDEDEDEDELELEVL 57

RESULT 3
US-10-821-234-1170
; Sequence 1170 Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pct Seq Genes Version 1.0
; SEQ ID NO 1170
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1170

Query Match      80.2%; Score 111.5; DB 6; Length 414;
Best Local Similarity 85.2%; Pred. No. 1e-05;
Matches 23; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EPEDEDEDEDEDEDEDEDEDEDELELEVL 27
Db 71 EPEDEDEDEDEDEDEDEDEDEDELELEVL 96

RESULT 4
US-11-044-899-29
; Sequence 29 Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
; APPLICANT: Schwab, M.
; APPLICANT: Chen, M.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
; FILE REFERENCE: 10200-017-999
; CURRENT APPLICATION NUMBER: US/11/044,899
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: 09/830,972
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/26160
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; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,446
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 1178
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...((1178) at all Xaa position
; OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-29

Query Match      80.2%; Score 111.5; DB 7; Length 1178;
Best Local Similarity 85.2%; Pred. No. 2.9e-05;
Matches 23; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 EPEDEDEDEDEDEDEDEDEDEDELELEVL 27
Db 30 EPEDEDEDEDEDEDEDEDEDEDELELEVL 55

RESULT 5
US-11-072-512-2973
; Sequence 2973 Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KENICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2973
; LENGTH: 683
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2973

Query Match      63.3%; Score 88; DB 7; Length 683;
Best Local Similarity 64.0%; Pred. No. 0.0059;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EPEDEDEDEDEDEDEDEDEDEDELELE 25
Db 333 EEEEDDEDEDEDEDEDEDEDELETESE 357

RESULT 6
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US-11-169-041-213
; Sequence 213, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-213
Query Match 63.3%; Score 88; DB 7; Length 773;
Best Local Similarity 64.0%; Pred. No. 0.0066;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPDEDEDEDEDEDEDEDELE 25
DB 485 EEEDEDEDEDEDEDEDELE 509
RESULT 7
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt-Seq_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443
Query Match 62.6%; Score 87; DB 6; Length 215;
Best Local Similarity 65.2%; Pred. No. 0.0023;
Matches 15; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 EPDEDEDEDEDEDEDELE 23
DB 190 DEDEDEDEDEDEDEED 212
RESULT 8
US-10-821-234-1413
; Sequence 1413, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia

FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt-Seq_genes Version 1.0
; SEQ ID NO 1413
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1413
Query Match 61.9%; Score 86; DB 6; Length 482;
Best Local Similarity 56.0%; Pred. No. 0.0068;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPDEDEDEDEDEDEDELE 25
DB 147 EEEDEDEDEDEDEDEDE 171
RESULT 9
US-11-072-512-2651
; Sequence 2651, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKANATSU, AI
; APPLICANT: SATO, HIROVUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2651
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2651
Query Match 61.9%; Score 86; DB 7; Length 687;
Best Local Similarity 56.0%; Pred. No. 0.0097;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPDEDEDEDEDEDEDELE 25
DB 124 EEEDEDEDEDEDEDEDE 148
RESULT 10
US-10-821-234-1254
; Sequence 1254, Application US/10821234

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; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1254
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1254

Query Match          60.4%; Score 84; DB 6; Length 144;
Best Local Similarity 56.0%; Pred. NO. 0.0033;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPDEDEDEDEDEDEDEDELEEE 25
DB      97 DDEDEDDDEDEDEDEDEDEEE 121

RESULT 11
US-10-528-031-8
; Sequence 8, Application US/10528031
; Publication No. US20050262577A1
; GENERAL INFORMATION:
; APPLICANT: ORDIS BIOMED Forschungs- und Entwicklungs GmbH
; APPLICANT: Guelly, Christian
; APPLICANT: Buck, Charles R.
; APPLICANT: Zatlouk, Kurt
; TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for b
; TITLE OF INVENTION: prevention, diagnosis or treatment of liver disorders and epithe
; FILE REFERENCE: Ordis Biomed
; CURRENT APPLICATION NUMBER: US/10/528,031
; CURRENT FILING DATE: 2005-03-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-528-031-8

Query Match          59.7%; Score 83; DB 6; Length 251;
Best Local Similarity 69.6%; Pred. NO. 0.0074; 3; Indels 0; Gaps 0;
Matches 16; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3 EDEDEDEDEDEDEDEDELEEE 25
DB      167 EEEDEGEDEDEDEDEDEEE 189

RESULT 12
US-11-024-959-415
; Sequence 415, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
US-11-024-959-415

Query Match          59.7%; Score 83; DB 7; Length 345;
Best Local Similarity 52.2%; Pred. NO. 0.01;
Matches 12; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY      1 EPDEDEDEDEDEDEDEDELEE 23
DB      175 EDEDEDEDEDEDEDEDEMKD 197

RESULT 13
US-11-054-281-107
; Sequence 107, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Metz et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/11/054,281
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 1229
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-054-281-107

Query Match          59.0%; Score 82; DB 7; Length 1229;
Best Local Similarity 65.2%; Pred. NO. 0.047;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPDEDEDEDEDEDEDEDELEE 23
DB      145 EEEEEEDEDEDEDEDDDDDE 167

RESULT 14
US-10-821-234-1536
; Sequence 1536, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
US-10-821-234-1536

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; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1536
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1536

Query Match      58.3%; Score 81; DB 6; Length 417;
Best Local Similarity 56.0%; Pred. No. 0.02;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EPDEDEDEDEDEDEDEDELELE 25
Db      381 EADKEDDEDEDEDEDEDEDE 405

RESULT 15
US-11-124-367A-293
; Sequence 293, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124.367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-124-367A-293

Query Match      58.3%; Score 81; DB 7; Length 740;
Best Local Similarity 51.6%; Pred. No. 0.036;
Matches 16; Conservative 7; Mismatches 2; Indels 6; Gaps 1;

Qy      1 EPDEDEDEDEDEDEDEDEDEDEDEDELELE 25
Db      441 EESDEDEDEDEDEDEDEDEDEDEDEDELE 471

Search completed: February 17, 2006, 04:03:51
Job time : 8.66667 secs
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